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**Contribution to the assessment of the risk of spreading banana
streak viruses (BSVs) in the Dominican Republic through the
cultivation of banana interspecific hybrids harbouring infectious
endogenous BSV sequences**

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Abstract

Endogenous Banana streak viruses (eBSVs) are present in the genome of *Musa balbisiana* spp. Some eBSVs are infectious and their activation by biotic and abiotic stresses lead to spontaneous infections by several species of *Banana streak virus* (BSV) in triploid (AAB) and tetraploid (AAAB) interspecific hybrids harboring the *M. balbisiana* genome. Although interspecific hybrids are grown over important areas in several countries throughout the Caribbean, Latin America and Africa, the risk of spreading BSVs associated to large scale cultivation of these hybrids has never been assessed.

This thesis focuses on the risk of spreading the three most widespread BSV species (BSOLV, BSGFV and BSIMV) in the Dominican Republic through the large scale cultivation of the two main banana hybrids that are grown in the country, Macho x Hembra, a natural triploid (AAB) plantain cultivar, and FHIA-21, a tetraploid (AAAB) hybrid.

An unprecedented survey was conducted throughout all the Dominican banana producing areas in order to assess the prevalence levels of BSOLV, BSGFV and BSIMV in MxH and FHIA-21 plantations. It showed that BSOLV and BSGFV are widespread in both varieties, with BSGFV being the most prevalent species, and that BSIMV is not present. BSGFV prevalence level was significantly higher in FHIA-21 than in MxH. Analyses of molecular taxonomical data of the natural mealybug vectors of BSVs and eBSV patterns of MxH and FHIA-21 were carried out and pointed to a marginal role of mealybugs in the transmission of BSGFV and BSOLV in the Dominican Republic in MxH and FHIA-21.

An experimental plot was set up and used for the first attempt ever made to monitor the kinetics of activation of infectious eBSOLV and eBSGFV in interspecific hybrids under field conditions. Results collected over a 15 months period showed that infectious alleles OL1 (eBSOLV) and GF7 (eBSGFV) are differentially expressed in MxH and FHIA-21, pointing to the existence of additional (plant) factors involved in the regulation of the expression of infectious eBSVs. They also showed that the mode of multiplication of the planting material influences activation levels. Preliminary results also suggest that BSV infection does not have a major effect on fruit production, although additional data are needed to reach definite conclusions in this regard.

Overall, this thesis contributes significantly to the development and implementation of appropriate strategies for evaluating and mitigating the risks of spreading BSVs that are associated with the cultivation of banana interspecific hybrids.

Keywords: Banana; interspecific hybrids; endogenous *Banana streak virus*; risk; prevalence; activation.

Résumé

Le génome *Musa balbisina* héberge des séquences virales endogènes du virus de la mosaïque en tirets du bananier (eBSV). Certaines de ces séquences sont infectieuses et leur activation par des stress biotiques ou abiotiques conduit à des infections spontanées par plusieurs espèces virales BSV dans les variétés hybrides triploïdes (AAB) ou tétraploïdes (AAAB). Bien que des variétés de ce type soient déployées à grande échelle dans de nombreux pays de la Caraïbe, d'Afrique et d'Amérique Latine, le risque de propagation des BSV lié à ce déploiement n'a jamais été évalué.

Cette thèse concerne l'évaluation du risque de diffusion en République Dominicaine de trois espèces virales BSV (BSOLV, BSGFV et BSIMV) lié à la culture à grande échelle des deux principales variétés hybrides cultivées dans le pays, Macho x Hembra (AAB) et FHIA-21 (AAAB).

Une étude de prévalence des espèces BSOLV, BSGFV et BSIMV de grande ampleur a été conduite dans l'ensemble des zones de culture de la banane en République Dominicaine sur les variétés MxH et FHIA-21. Elle a montré que les espèces BSOLV et BSGFV sont très présentes dans les deux variétés, que l'espèce BSGFV présente les niveaux de prévalence les plus élevés dans ces variétés et que ce niveau est significativement plus élevé chez FHIA-21 que chez MxH. Les résultats d'analyses de taxonomie moléculaire conduites sur les cochenilles, dont certaines espèces sont des vecteurs des BSV, et de caractérisation moléculaire des allèles infectieux OL1 (eBSOLV) et GF7 (eBSGFV) présents chez MxH et FHIA-21 suggèrent que la transmission des espèces virales BSOLV et BSGFV chez MxH et FHIA-21 résulte principalement de l'activation de ces allèles infectieux plutôt que d'une transmission vectorielle par cochenille.

Une expérimentation au champ a été mise en place afin d'étudier pour la première fois la cinétique d'activation des allèles infectieux OL1 et GF7 dans des variétés hybrides interspécifiques en conditions de culture au champ. Les résultats obtenus au terme d'une période de suivi de 15 mois montrent que les allèles infectieux OL1 et GF7 ne sont pas exprimés au même niveau ni dans les variétés MxH et FHIA-21, qui présentent pourtant des profils alléliques eBSOLV et eBSGFV strictement identiques, ni pour une même variété (FHIA-21) selon le mode de multiplication utilisé pour générer les plants de l'essai. Ces données étayent l'hypothèse déjà formulée qu'un (ou des) facteur(s) autres que les allèles eBSV infectieux sont nécessaires à l'expression de ces allèles. Des résultats préliminaires issus de l'essai au champ suggèrent également que les infections par les espèces BSOLV et BSGFV n'ont que peu d'incidence sur la production fruitière chez les variétés MxH et FHIA ; cependant la faiblesse de l'échantillonnage ne permet pas encore d'étayer suffisamment ces résultats pour pouvoir conclure sur cet aspect.

Globalement, cette thèse apporte une contribution significative à l'évaluation et à la gestion du risque BSV associé à la culture à grande échelle de variétés interspécifiques de bananier, notamment par la mise au point d'approches d'évaluation de ce risque transposables à d'autres variétés.

Mots clés : bananier ; hybride interspécifique ; séquence BSV endogène ; risque ; prévalence ; activation

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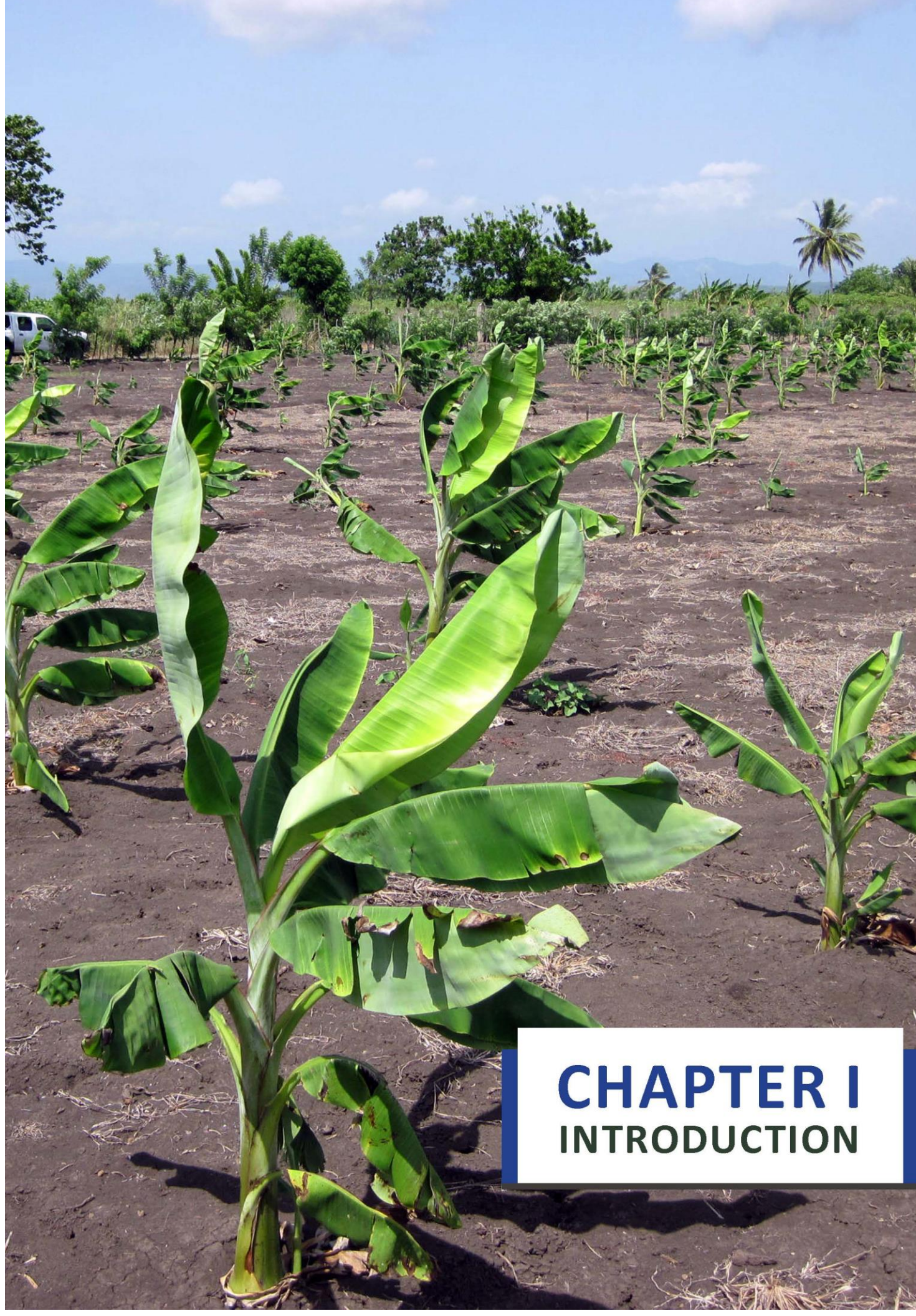
List of abbreviations and acronyms

DNA	Desoxyribonucleic acid
AntiBSV	Anti-BSV polyclonal antiserum
AP	Aspartic protease
RNA	Ribonucleic acid
ARNpg	pregenomic RNA
BEL	BSV expressed locus
BSA	Bovin serum albumin
Blast	Basic Local Alignment Search Tool
BSD	Banana streak disease
CIRAD	Centre de Coopération Internationale en Recherche Agronomique pour le Développement
dCAPS	Derived cleaved amplified polymorphic sequences
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuaria
EVE	Endogenous viral element
eBSV	Endogenous BSV sequence
EDTA	Ethylene diamine tetra-acetic acid
TE	Transposable element
ELISA	Enzyme linked immunosorbent assay
EPRV	Endogenous pararetrovirus
FISH	Fluorescent <i>in-situ</i> hybridization
FHIA	Honduran Foundation for Agricultural Research
GRD	Geminivirus-related DNA
HGT	Horizontal gene transfer
ITFRI	Indonesian Fruits Research Institute
IC-PCR	Immunocapture polymerase chain reaction
ICTV	International Committee for the Taxonomy of Viruses
IITA	International Institute of Tropical Agriculture
ITC	Musa international transit center
ITS	Internal transcribed spacer
kbp	kilobase pair
LTR	Long Terminal Repeat
M-IC- PCR	Multiplex Immunocapture PCR
MP	Movement Protein
NARO	National Agricultural Research Organisation

NRCB	National Research Centre for Banana
ORF	Open Reading Frame
PCR	Polymerase chain reaction
PKW	Pisang Klutuk Wulung
PBS-T	Phosphate buffer saline-Tween 20
STMS	Sequence tagged microsatellite
RB	RNA binding domain
RH	RNase H
RCA	Rolling circle amplification
RFLP	Restriction Fragment Length Polymorphism
RT	Reverse transcriptase

List of viruses

ABrMV	<i>Abacá bract mosaic virus</i>
AbBTv	<i>Abacá bunchy top virus</i>
BanMMV	<i>Banana mild mosaic virus</i>
BSVNV	<i>Banana streak Vietnam virus</i>
BSAcYunV	<i>Banana streak acuminata Yunnan virus</i>
BBrMV	<i>Banana bract mosaic virus</i>
BBTV	<i>Banana bunchy top virus</i>
BSGFV	<i>Banana streak Goldfinger virus</i>
BSIMV	<i>Banana streak Imove virus</i>
BSOLV	<i>Banana streak Obino l'Ewaï virus</i>
BSUAV	<i>Banana streak UA virus</i>
BSUIV	<i>Banana streak UI virus</i>
BSULV	<i>Banana streak UL virus</i>
BSCAV	<i>Banana streak CA virus</i>
BSUMV	<i>Banana streak UM virus</i>
BVX	Banana virus X
CaMV	<i>Cauliflower mosaic virus</i>
CMV	<i>Cucumber mosaic virus</i>
CSSV	<i>Cacao swollen shoot virus</i>
DBV	<i>Dioscorea bacilliform virus</i>
DMV	<i>Dahlia mosaic virus</i>
ePVCV	Endogenous petunia vein clearing virus
eBSGFV	Endogenous banana streak Goldfinger virus
eBSOLV	Endogenous banana streak Obino l'Ewaï virus
eBSIMV	Endogenous banana streak Imove virus
eTVCV	Endogenous tobacco vein clearing virus
RTBV	<i>Rice tungro bacilliform virus</i>
PVCV	<i>Petunia vein clearing virus</i>
SCBV	<i>Sugarcane bacilliform virus</i>
SCMV	<i>Sugarcane mosaic virus</i>
SCMV-Ab	<i>Sugarcane mosaic virus, abacá strain</i>



CHAPTER I

INTRODUCTION

I-1. Banana, a giant herbaceous plant that successfully conquered the tropics and subtropics

I-1.1. Morphology and life cycle of banana plants

Banana is the largest herbaceous flowering plant on earth, with some wild species reaching up to 9m in height while the average size of cultivated species is rather in the 3-5m range. Contrary to widespread belief, banana has no lignified part and is therefore not a tree. Its pseudostem (Figure I-1) is made of successive tightly packed leaf sheaths that are emitted from the apical meristem located at the center of this pseudostem. Leaf emission rates depend on cultivars and growing conditions, reaching up to 3.8 leaves per month, for Cavendish banana under tropical summer conditions (Jones, 2000). Leaves are composed of a petiole and a lamina and can reach several square meters in surface, ensuring an active photosynthetic activity despite being often torn by the wind. A subterranean rhizome called corm supports all the aerial parts of the plant.

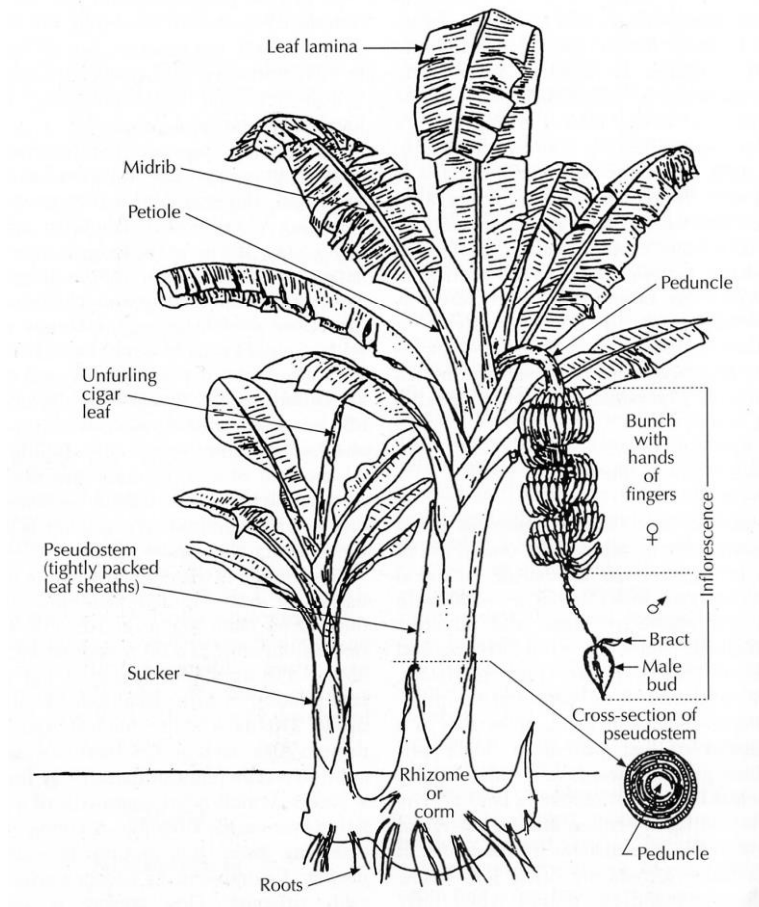


Figure I-1: Schematic representation of a banana plant.

From Champion 1963

When mature, banana stops emitting new leaves and form a single inflorescence that emerges from the top of the pseudostem along a peduncle. The inflorescence is protected by thick purple and rubbery bracts, which progressively dry and fall off, exposing tightly packed female flowers that will develop in fingers (fruits) arranged in one bunch, then male flowers. This non simultaneous emission of the female and male flower limits self-pollination. Plants die following bunch harvest, but suckers are constantly emitted by the corm through vegetative propagation. These suckers take over and grow new plants, therefore banana is considered perennial. For cultivated banana, farmers select one of the suckers as daughter plant and cut off other suckers to fasten the next fruit production cycle by channeling water and nutrients to the daughter plant only.

I-1.2. Taxonomic classification of *Musa* spp

Banana is a monocotyledonous flowering plant that belongs to the genus *Musa* of the family *Musaceae*, in the order *Zingiberales*. The *Musaceae* family comprises the Asian and African genus *Ensete*, the Asian genus *Musella*, and the East Asian genus *Musa* (Delanghe *et al.*, 2009; Perrier *et al.*, 2011). Based on morphological and cytological criteria, the genus *Musa* has been subdivided into five sections: *Eumusa* and *Rhodochlamys* whose members have 22 chromosomes ($2n = 22$); *Australimusa* and *Callimusa* whose members have 20 chromosomes ($2n = 20$); *Ingentimusa*, whose only member, *Musa ingens*, has 14 chromosomes ($2n=14$). However, based on molecular phylogenetic studies of chloroplast and nuclear ribosomal cistron internal transcribed spacer (ITS) sequences, Li *et al* (2010) proposed to group sections *Australimusa*, *Callimusa* and *Ingentimusa* in the same monophyletic clade (Figure I-2; clade I) and to group *Eumusa* and *Rhodochlamys* in a separate but also monophyletic clade (Figure I-2; clade II).

I-1.3. Origin and spread of cultivated *Musa* spp

Edible banana arose from a series of wild *M. acuminata* diploid (AA) subspecies originating from various locations throughout South East Asia (Simmonds, 1962; Figure I-3). Molecular and ethno biological analyses showed that *M. acuminata* subspecies were brought into contact by human movement in South East Asia and western Melanesia probably during the Holocene –which started ca 11,700 years ago- leading to edible diploid AA cultivars through hybridization (Perrier *et al.*, 2011). These contacts also allowed hybridizations between diploid *M. acuminata* landraces and diploid *M. balbisiana* (BB) to take place in areas of South East Asia where *M. balbisiana* is also endemic (Fig. I-3), giving rise to interspecific AB hybrids harboring both the *M. acuminata* and *M. balbisiana* genomes. With the acquisition of drought tolerance traits brought by *M. balbisiana*, these interspecific hybrids were instrumental in the extension of banana cultivation to drier zones where rainfalls are only seasonal.



Figure I-2: *Musaceae* phylogenetic tree inferred from the combined analyses of nuclear ITS and chloroplast sequences.

The numbers above the branches are respectively the maximum parsimony bootstrap support and Bayesian posterior probabilities. The two main clades of *Musa* and the suggested basic chromosome numbers ($x = 11$, $x = 10/9/7$) are plotted onto the relevant clades. From Li et al., 2010

Considering that wild banana species are seedy, it is likely that the first steps in domestication were the selection of plants with high levels of parthenocarpy and female sterility producing seedless fruits, and their propagation by suckers. Another important step in the evolution of banana occurred when haploid pollen fertilized diploid egg cells, giving rise to triploid AAA, AAB and ABB cultivars (Figure I-4) that are bigger than diploid ones and produce larger fruits (Perrier et al., 2011).

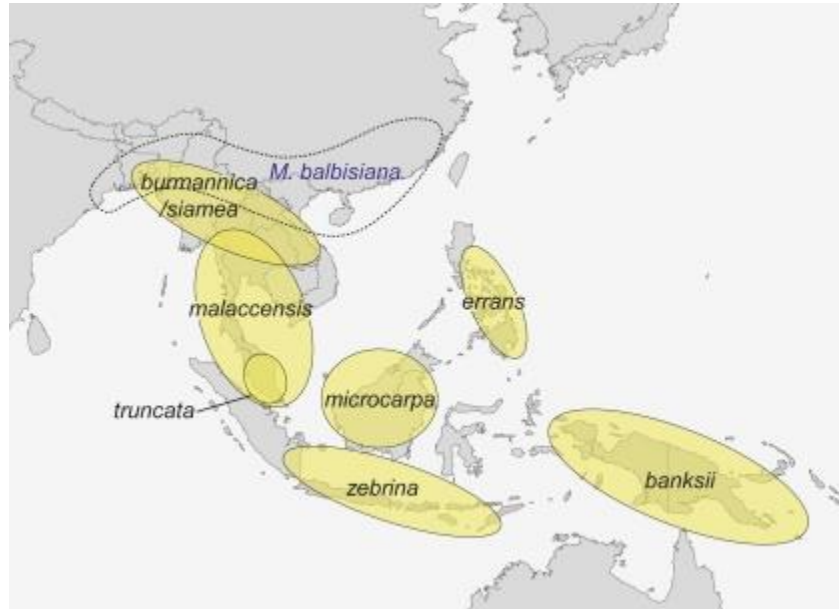


Figure I-3: Geographical distribution of the wild ancestors of cultivated bananas, based on nuclear and cytoplasmic markers analyses.

From Perrier et al., 2011

From then on, banana embarked in mankind's travel bags on a journey that saw it conquer all tropical and subtropical regions. The mode of dispersal (terrestrial vs maritime) from Asia to Africa has not been elucidated yet (De Langhe, 2007; Blench, 2009). On the contrary, there is ethnobotanical evidence that what is now referred to as AAB Pacific plantains were spread across Pacific islands by Austronesian-speaking colonists (Perrier *et al.*, 2011). Moreover, it is likely that African plantain cultivars were introduced to South India with the East African slave trade (Perrier *et al.*, 2011). In his record of Spanish conquest of the West Indies ("*La historia general y natural de las Indias*"), historian Gonzalo Fernández de Oviedo y Valdés (1478 – 1557) reports that it is Reverend Fray Tomas de Berlanga, who introduced *Musa* ssp. to Hispaniola (now split between the Dominican Republic and Haiti) from the Canary Islands in 1516; T. de Berlanga also spread this crop to other islands in the Caribbean and to tropical America, paving the way to one of the most successful examples of crop introduction in agriculture's history.

I-1.4. Why banana became a success

The main reason why banana was rapidly adopted upon its introduction in the tropics and subtropics lies in nutrition facts: fruits are rich in carbohydrates, fibers and minerals such as potassium. Originally a weed, banana is a very robust and not very demanding crop. It can grow and bear fruits with minimal care in a wide range of soil types, although fertilization can increase yields substantially. Banana can also be grown in association with other crops to which it brings shade.

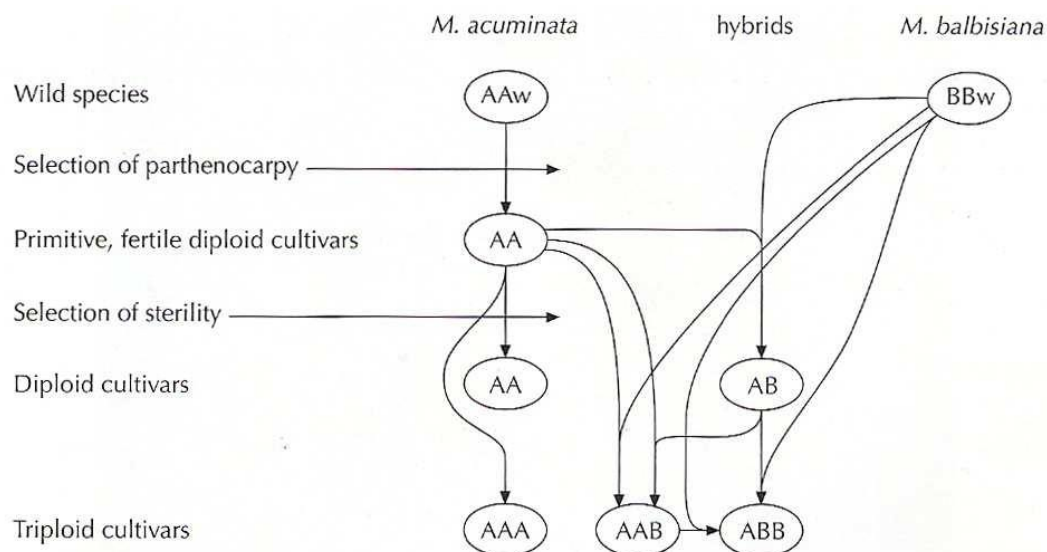


Figure I-4: Main steps in the evolution of edible banana cultivars from the wild species *M. acuminata* and *M. balbisiana*.

From Jones, 2000.

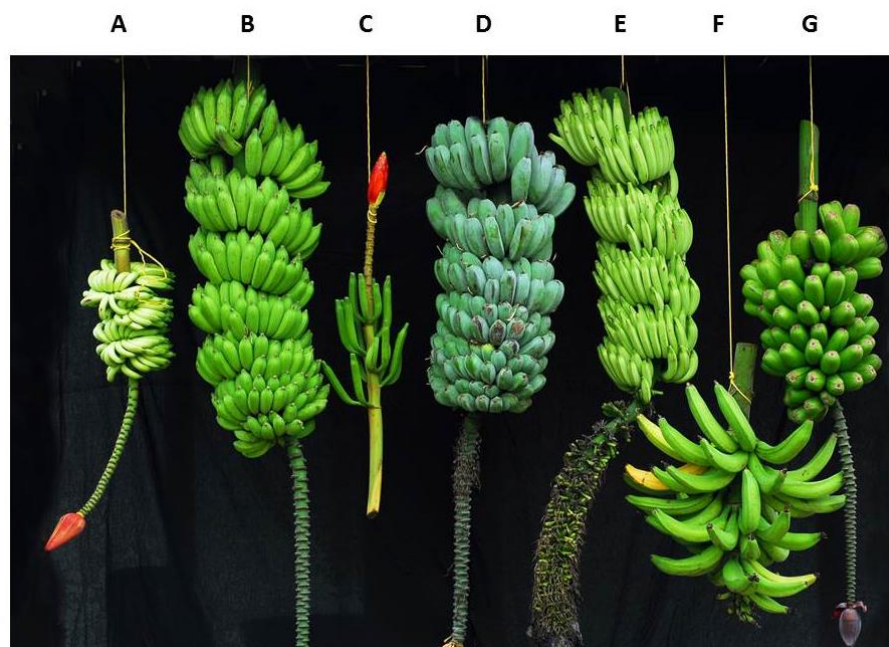


Figure I-5: Morphological diversity of banana fruits.

A: Selangor (*Musa acuminata* subsp. *Malaccensis*) ; B: Pisang Ceylan (AAB) ; C: *Musa becarii* (ornamental) ; C: Butuhan (wild BB) ; D: Pisang Jari Buaya (AA cv) ; E: Curare Enano (AAB plantain type) ; F: Popoulou (AAB).

© P. Fournier, CIRAD

Another reason for its success lies in the remarkable diversity in fruit sizes, tastes and starch contents, which can suit the diversity in consumer's tastes and cooking uses (Figure I-5). This diversity increases during cultivation since banana is prone to spontaneous mutations and epigenetic variations that result in somaclonal variants with modified phenotypic traits (Pollefeys *et al.*, 2004; Heslop-Harrison & Schwarzacher, 2007).

Also, banana is extremely versatile: all parts of the plant can be used. Fruits can be processed in many different ways for human consumption: they can be eaten raw, boiled, fried, dried, turned into chips or into flour, fermented to make beer; bracts can also be eaten raw; leaves can be used as wrapping material for cooking or as plates; the pseudostem can be mulched to feed animals or used for extracting fibers that can be used to make textiles or non-putrescible ropes; even seeds can be used to make jewels. All byproducts can also be recycled for a variety of uses including thickening agent, coloring and flavor, nutraceuticals and natural bio-fertilizer (Padam *et al.*, 2014).

I-2. Banana, an essential crop to world food security and economy

I-2.1. Worldwide production, trade and socio-economic importance

Banana is one of the major food commodities after rice, wheat and maize and is the fourth largest fruit export trade worldwide (FAO, 2014), with an estimated annual production of 133MT (Lescot 2015; Table I-1). It is estimated that 150 countries around the world produce bananas (FAO, 2014). Banana is the world's most exported fresh fruit both in volume and value (US\$7bn/year), representing an essential source of income and employment for hundreds of thousands of rural households in developing countries. Consumption per capita vary to a large extent between countries: it can reach 250 kilos per year in the Great Lakes region of East Africa, and in the island of New Guinea, where banana is a major staple food and brings most of the daily food intake, whereas figures are in the 15 kilos per person and per year in Europe where banana is consumed occasionally as a fruit (Jones, 2000).

Table I-1 shows the most recent figures for the production and trade of banana worldwide (Lescot, 2015). Cooking bananas represent roughly 41% of the world production of banana, and dessert banana the remaining 59%. Interestingly, although almost 34% of the world production of Cavendish banana is traded, only 4% of the plantain production is. This unbalance shows that dessert banana is an important cash crop grown for export and plays a key role in the export balance trade of many countries in the tropics and subtropics. On the opposite, plantain is essentially a staple food grown for local consumption, although its role in local economies is vital to millions of small scale farmers.

Table I-1: World banana production and trade in years 2013/2014*Estimates are given in tons*

	Production					Export				
	Cooking bananas		Dessert bananas		Total	% of total	Cavendish	Plantain	Total	% of total
	Plantain AAB group	Highland bananas + ABB group + others	Cavendish	Gros Michel + others						
North America	0	1 000	6 525	100	7625	0,01%	545 149	16 306	561 455	2,56%
South America	5 607 796	388 856	13 049 085	3 410 650	22456387	16,80%	7 388 154	356 724	7 744 878	35,30%
Central America	808 338	62 455	7 390 999	71 500	8333292	6,23%	5 277 927	310 663	5 588 590	25,47%
Caribbean	767 852	665 957	1 096 248	168 887	2698944	2,02%	637 209	5 848	643 057	2,93%
West and Central Africa	9 468 569	1 247 796	2 401 702	498 442	13616509	10,18%	512 157	78 454	590 611	2,69%
East Africa	966 418	15 785 050	3 519 093	893 683	21164244	15,83%	204 152	3 006	207 158	0,94%
North Africa and Middle East	33	9 067	2 226 494	71 882	2307476	1,73%	122 174	0	122 174	0,56%
Asia	2 113 680	16 406 438	31 098 370	11 460 263	61078751	45,69%	3 473 967	26 068	3 500 035	15,95%
Oceania	1 162	530 706	796 437	276 486	1604791	1,20%	1 161	0	1 161	0,01%
Europe	2	17	423 900	27	423946	0,32%	2 900 141	83 523	2 983 664	13,60%
Total	19733850	35097342	62008853	16851920	133691965	100,00%	21 062 191	880 592	21 942 783	100,00%
	14,76%	26,25%	46,38%	12,61%			95,99%	4,01%		
	*	*	*	*			**	**		

*: expressed as a percentage of total production

**: expressed as a percentage of total exports

Modified from Lescot, 2015; © Fruitrop, CIRAD.

However, situations differ between regions. South and Central America are the main contributors to banana exports: they export respectively 56.6% and 71.41% of their production of Cavendish banana. In comparison, Asia exports only 11.17% of its production of Cavendish banana. Taken together, South and Central America account for 23.03% of the overall world production of banana and for 60.77% of the world exports; again in comparison, Asia accounts for 45.69% of the overall world production but only for 15.95% of the world exports, whereas the figures for Africa are 26.01% and 3.64%, respectively.

Worldwide banana production has been rising steadily for the past 25 years in all production areas (Fig I-6), increasing more than two folds over that period in order to respond to the constantly growing demand resulting from human population growth. This remarkable achievement results from an increase of both the cultivated surfaces, yields (FAO, 2014), and shows that banana remains one of the most important crops for worldwide food security.

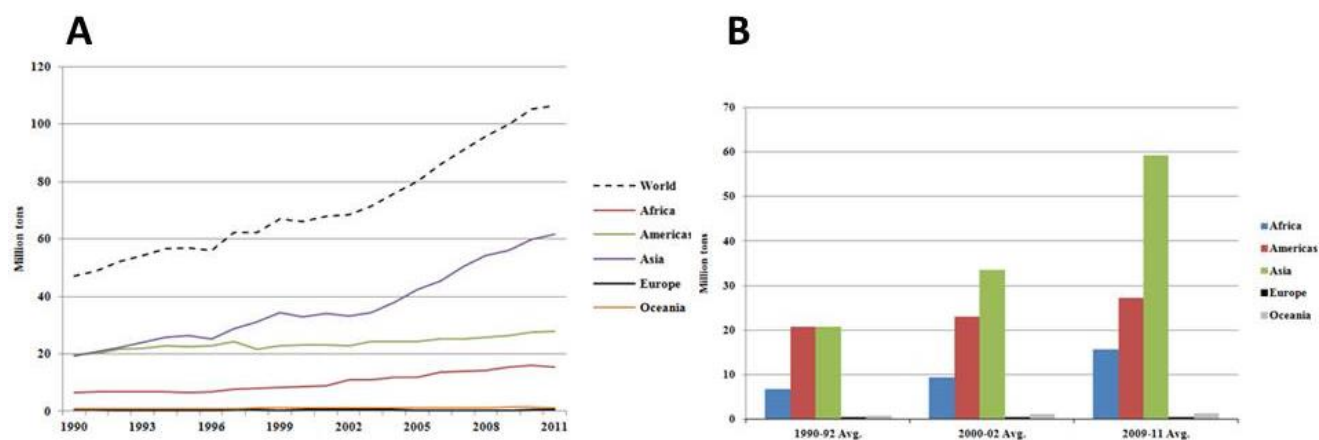


Figure I-6: Evolution of banana production worldwide between 1990 and 2011

A: overall evolution

B: comparative evolution of the production in Africa, the Americas and Asia

From FAO, 2014

I-2.2. Banana in the Dominican Republic

The Dominican Republic is the perfect illustration of the dual role of banana as a cash crop and a subsistence crop. The country is self-sufficient and a net exporter of both dessert banana and plantain and it is currently the largest Caribbean exporter. Cooking type bananas represent 44.13% of the production and dessert banana the remaining 55.87%. The largest part of plantain production is for local consumption, with only 1.66% being exported. On the opposite, about two thirds (65.72%) of the Cavendish production is exported. Overall, 36.9% of the whole Dominican production is exported, generating an annual income of US \$200 million, whereas annual consumption per capita stands at 59 kilograms.

Like other Caribbean countries, the Dominican Republic joined the African, Caribbean, and Pacific (ACP) Group of States in 1990, and benefits from the duty free export of bananas into the European Union ever since. This preferred status has boosted production and exports to the EU, which has become its main export market, now representing 80% of its exports. One of the other specificities of the Dominican Republic is that it has been a pioneer in the production and export of organic banana, a very lucrative export market. To date the country remains by far the largest producer and exporter of organic banana worldwide and its main export markets are Germany, The Netherlands and the United Kingdom.

Table I-2: Banana production and trade in the Dominican Republic in years 2013/2014

Estimates are given in tons

Production					Export		
Cooking Bananas		Dessert bananas		Total	Cavendish	Plantain	Total
Plantain AAB group	Highland bananas, + ABB group + others	Cavendish	Gros Michel + others				
229 055	200 000	540 000	3 000	972 055	354 872	3 804	358 676
23,56%	20,57%	55,55%	0,31%	100,00%	65,72%	1,66%	
*	*	*	*		**	**	

*: expressed as a percentage of total production

**: expressed as a percentage of the production of Cavendish and plantain, respectively

Modified from Lescot, 2015; © Fruitrop, CIRAD.

In the Dominican Republic, banana is mainly produced by small and medium scale farmers as a subsistence crop and a cash crop. Therefore, banana cultivation and trade not only generates jobs and income for rural communities but it also plays a central role in the country's socio economic balance through its contribution to food security and to reduce rural poverty. Banana is grown throughout the country, but most of the production comes from the northern Valle del Cibao, which concentrates 54% of the national areas devoted to banana cultivation, the Southern Region (31%) and the Northwest Region in Western Cibao Valley (5%) (IICA, 2008).

A large number of banana varieties and cultivars is grown in the Dominican Republic. Macho x Hembra, a local triploid AAB cultivar, and FHIA21, a tetraploid AAAB hybrid, are the two main cooking types grown in the country. Other cooking types grown to a lesser extent include French type and horn type plantains (AAB), tetraploid AAB hybrid FHIA-03 and triploid hybrid FHIA-25 (AAB). Likewise, giant dwarf Cavendish (AAA) is the main dessert type grown essentially for export. Other dessert types include Valery (AAA), Gros Michel (AAA) and hybrids FHIA18 (AAAB), and FHIA 20 (AAAB).

I-3. Main pests and diseases of banana

All living organisms are the prey of pests and pathogens, and banana is no exception. Pests and diseases are particularly problematic when banana is grown as a monoculture on extended surfaces that offer ideal conditions for their spread. This is especially true of Cavendish cultivars, which are grown as monoculture in all big producing countries and are particularly vulnerable to diseases since they are related clones with no genetic diversity.

I-3.1. Main pests

I-3.1.1 Banana weevil (*Cosmopolites sordidus*)

C. sordidus larvae preferentially feed in the rhizome, but also attack the true stem and, occasionally, the pseudostem digging holes and galleries (Figure I-7A), therefore hampering plant nutrition (Njau *et al.*, 2011) and providing entry for rot-promoting organisms. In the early stages of infestation, plants lose vigor. As insects multiplies in the corm, symptoms increase, including tapering of the stem, reduction in leaf size, poor bunch formation and choked throat appearance due to grub damage in corms, eventually leading to plant death (Pinese & Elder, 2004). Impact on production of all types of banana can be very important: losses of more than 40% of the plant crop have been reported, resulting from both plant loss (plant death, rhizome snapping, toppling) and lower bunch weights.

Therefore, weevil is considered the major constraint to banana production worldwide. Weevils spread through the movement of infested suckers (Coto and Saunders, 2004). Control strategies include the use of clean planting material, cultural practices, chemical control when infestation levels are high, use of more environment-friendly pheromone traps, which have proved very efficient to control weevil populations when infestation levels are low to medium (Gold *et al.*, 2001).

I-3.1.2 Burrowing nematode (*Radopholus similis*)

R. similis is a migratory endoparasitic nematode, which invades banana's root and corm tissues from the soil (Chabrier *et al.*, 2010). They feed on the cytoplasm of cortex cells and cause the collapse of cell walls, which result in cavities and tunnels, eventually causing root and corm necrosis, which in turn become entry routes for fungal and bacterial pathogens. Damage to the root system reduces water and mineral uptake, causing a reduction of plant growth, and increase uprooting and toppling of plants during strong winds and heavy rain periods. Losses up to 75% have been reported in Côte d'Ivoire, although average losses to burrowing nematode are more frequently in the 15% range. *R. similis* is present in all banana producing areas, and is considered a major constraint to banana production worldwide.

Control strategies include reducing nematode populations in the soil before planting, for example by conducting a fallow or cultivation of non-host plants prior to planting banana, the use of nematicides, which are very polluting and prohibited in several countries, or the use of resistant or tolerant cultivars.



Figure I-7: Damage caused on banana corm by *C. sordidus* (A) and on a banana root by *R. similis* (B)

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I-3.2. Main fungal diseases

I-3.2.1 Fusarium wilt

Fusarium wilt is a vascular wilt disease caused by the fungus *Fusarium oxysporum*. A tropical race 4 (TR4) of *Fusarium oxysporum* f. sp. *cubense* (Foc) emerged in South East Asia in the late 1980's and is devastating Cavendish plantations (Molina, 2009; Pocasangre, 2009), which are otherwise resistant to Panama disease caused by a different race (race 1) of the fungus. In less than 20 years, TR4 has spread to Western Asia, Australia and Africa (Ploetz, 2015), and there is fear that it could spread to South America, where it has the potential to wipe out the banana industry. Symptoms of TR4 are similar to those caused by Panama disease; the main difference between those two races is that TR4 has a much wider host range. The fungus invades the vascular system through the roots, and then spreads to the rhizome and to the pseudostem. It causes leaf yellowing, causing the leaves to collapse and dry.

Infected plants die in a few months only. Since the fungus survives for years in soils, is spread by run-off water and transmitted to suckers, its spread is very fast, long lasting and very efficient. No chemical control is available; therefore, control strategies rely on the use of clean planting material and strong quarantine regulations.

I-3.2.2 Black Sigatoka

Black Sigatoka is the most devastating fungal leaf disease of banana. It is caused by the fungus *Mycosphaerella fijiensis*. Since it was reported for the first time in the Sigatoka valley in Fiji in the 1960's, it has spread worldwide to all banana growing areas probably through a complex scenario involving multiple introduction events in the Americas and a single introduction event in Africa (Robert *et al.*, 2012).

Infected plants develop leaf streaks that progressively invade the whole surface of leaves and become necrotic, causing an important decrease in photosynthetic activity and disorders in fruit ripening that severely affect the market value of the fruits. Disease control currently relies on the use of fungicides, which are too expensive for

small scale farmers and lead to the emergence of resistance among fungal populations, pushing to apply more fungicides more often therefore increasing the impact on the environment and public health. More sustainable and environmentally friendly approaches are being developed, such as breeding resistant hybrid varieties (see below I-4-1).

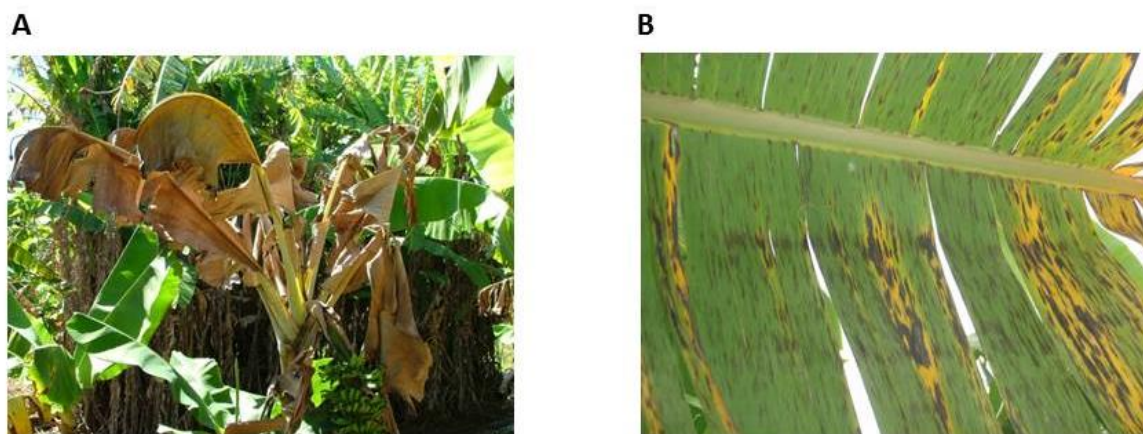


Figure I-8: General necrosis caused by *F. oxysporum* TR4 (A) and leaf symptoms caused by *M. fijiensis* (B)

© Australia Northern Territory Government (A) and T. Lescot, CIRAD (B)

I-3.3. Main bacterial diseases

I-3.3.1 Moko disease

Moko Disease, also known as bacterial wilt, is caused by several strains of *Ralstonia solanacearum* (race 2, biovar 1) which evolved from strains infecting native *Heliconia* in the Americas upon the introduction of banana (Buddenhagen, 1961). It is considered the most important bacterial disease of banana (Jones, 2000) and is the principal bacterial constraint to plantain production in Latin America and the Caribbean. Disease symptoms include yellowing and wilting of leaves that eventually die and collapse, discoloration of leaf and fruit stems, premature development and splitting of fruits. Uneven premature ripening of fingers occurs on Cavendish cultivars. Fruits become progressively discolored then brown or grey, and rot (Figure I-9A).

R. solanacearum can survive in soils for over 18 months and all year round in plant parts such as roots, stems, bunches, fruit, peel, suckers and leaf material, making them important sources of inoculum. Bacteria can be spread on hands, tools, machinery, shoes, by animals and in run off water and spread by contaminated fruit shipments. It is primarily spread between farms and beyond via contaminated planting material; therefore the most efficient control measure is the use of clean planting material.

I-3.3.2 Xanthomonas wilt

Xanthomonas wilt is caused by *Xanthomonas campestris* pv. *musacearum*. It was first detected in Ethiopia on *Ensete* (Bradbury & Yiguro, 1968) then re-emerged in Uganda on all types of banana (Tushemereirwe *et al.*, 2004). It has since spread throughout Central and East Africa, where it causes yield losses up to 52% and is now considered a major threat to food security in the region (Karamura *et al.*, 2011). The disease causes leaf

yellowing and general necrosis that eventually leads to the death of infected plants. It also causes rotting of the fruit (Figure I-9B).

The disease is transmitted by insects, farm tools, water run-off and splashing (Vivas *et al.*, 2009). Short and long distance spread is associated with the movement of infected suckers for replanting. Control measures include removal of infected plants upon the appearance of the first symptoms and use of clean planting material.



Figure I-9: Symptoms on fruits caused by Moko disease (A) and *Xanthomonas* wilt (B)

© Promusa

I-3.4. Main viral diseases

Although viruses are not the main phytopathological constraints for banana production worldwide, some of them are at local or regional levels, causing yield losses to such an important level that they threaten food security over entire geographic zones. Table I-3 provides an extensive overview of all viruses known to occur on banana. The list is relatively short when compared to the number of viruses infecting other vegetatively propagated tropical crops of equivalent or lower importance such as yams or cassava e.g., and even recent metagenomics studies failed to unveil additional viruses infecting bananas (Teycheney, pers. comm).

Following the recent review published by Lava *et al.* (2015), we can distinguish between viruses of significant economic importance (BBTV, AbBTV, BBrMV and BSVs), which are detailed below, and viruses of minor economic importance (BanMMV, BVX, SCMV and CMV).

Since BSVs are the topic of this thesis, they are developed in a separate section of this chapter (see I-3-5. below).

Table I-3: viruses known to occur in banana (*Musa spp*)

Virus Name	Taxonomy			Transmission mode		References
	Acronym	Family	Genus	Vector-mediated	Other	
<i>Abacá bunchy top virus</i>	AbBTv	<i>Nanoviridae</i>	<i>Babuvirus</i>	Non persistent by aphid species <i>P. nigronervosa</i>	Infected plant material, vegetative propagation	Ocfemia, 1930; Sharman <i>et al.</i> , 2008
<i>Banana mild mosaic virus</i>	BanMMV	<i>Betaflexiviridae</i>	Unassigned	Unknown	Infected plant material, vegetative propagation	Gambley & Thomas, 2001; Teycheney <i>et al.</i> , 2005a
<i>Banana bract mosaic virus</i>	BBrMV	<i>Potyviridae</i>	<i>Potyvirus</i>	Non persistent by several aphid species	Infected plant material, vegetative propagation	Thomas <i>et al.</i> , 1997
<i>Banana bunchy top virus</i>	BBTV	<i>Nanoviridae</i>	<i>Babuvirus</i>	Non persistent by aphid species <i>P. nigronervosa</i>	Infected plant material, vegetative propagation	Dale, 1987
<i>Banana streak viruses</i>	BSV	<i>Caulimoviridae</i>	<i>Badnavirus</i>	Several mealybug species	Infected plant material, vegetative propagation, infectious eBSVs	see Table I-4
<i>Banana virus X</i>	BVX	<i>Betaflexiviridae</i>	Unassigned	Unknown	Infected plant material, vegetative propagation	Teycheney <i>et al.</i> , 2005b
<i>Cucumber mosaic virus</i>	CMV	<i>Bromoviridae</i>	<i>Cucumovirus</i>	Non persistent by several aphid species	Infected plant material, vegetative propagation	Jones, 2000
<i>Sugarcane mosaic virus, abacá strain</i>	SCMV-Ab	<i>Potyviridae</i>	<i>Potyvirus</i>	Non persistent by several aphid species	Infected plant material, vegetative propagation	Eloja & Tinsley, 1963

I-3.4.1 *Banana bunchy top virus* (BBTV) and *Abacá bunchy top virus* (AbBTv)

BBTV is the most devastating virus infecting banana. Since it was first encountered in Fiji in 1885, it has spread to Southeast Asia, the South Pacific, parts of India, Africa and Australia. Noticeably, Central and South America and the Caribbean are still free of BBTV. BBTV is very efficiently transmitted by the aphid species *Pentalonia*

nigronervosa in a non-persistent manner. Medium and long distance spread of the virus is mediated by the exchange of infected planting material such as suckers (Kumar *et al.*, 2011).

Infection causes typical symptoms including progressive dwarfism of leaves, which become upright and bunched at the top of the plant (Figure I-10A) and display chlorotic margins that tend to turn necrotic. However, symptoms occurring early in the infection process, such as 'Morse code' patterns on the leaves, are more difficult to identify, therefore infections often go unnoticed for several months. Infected plants are stunted and rarely bear fruits, and plant death occurs in a matter of months. BBTV severely reduces yields wherever it occurs (Lava *et al.*, 2015). Its current spread in West Africa is of particular concern to food security in this area, where banana is one of the most important food crops. There is currently no cure for BBTV. Immediate eradication of infected plants and use of clean planting material are the only way to control virus spread. In 2008, Sharman *et al.* characterized two isolates of a new virus closely related to BBTV, for which they proposed the name Abacá *bunchy top virus* (AbaBTV). One isolate infected abacá (*Musa textilis*) in the Philippines and one infected banana in Malaysia, and both displayed symptoms similar to those caused by BBTV.

I-3.4.2 Banana bract mosaic virus (BBrMV)

Since its first detection in the Philippines in 1979 (Magnaye *et al.*, 1990), BBrMV has spread to other Asian countries, the Pacific and South America (Lava *et al.*, 2015). There is serious concern that it may spread further to important production zones of South America. Infection has a serious impact on fruit production, causing reduced bunch weights, malformed bunches and underdeveloped fingers. The most distinctive symptom is a dark reddish-brown mosaic pattern on flower bracts (Figure I-10B), that appear late in the life cycle of bananas and hampers visual diagnostic, since leaf and stem symptom, which appear at earlier development stages, are difficult to identify. BBrMV is transmitted non-persistently by at least three aphid species (*Pentalonia nigronervosa*, *Aphis gossypii* and *Rhopalosiphum maidis*) and vegetatively through contaminated planting material. As for all other viruses infecting *Musa* spp, control strategies rely on the use of clean planting material and on the eradication of infected plants.

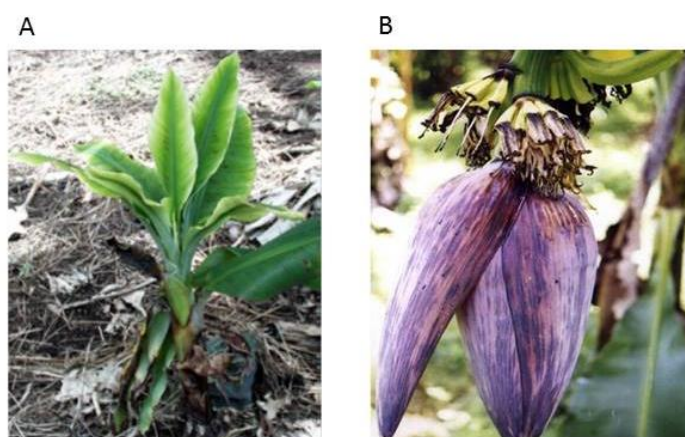


Figure I-10: Bunching symptoms of BBTV (A) and bract mosaic symptoms of BBrMV (B).

© American Samoa Community College (A) & M.-L. Iskra Caruana, CIRAD (B).

I-3.5. Banana streak viruses

I-3.5.1. Symptomatology, prevalence and impact on production

Banana streak disease (BSD) is caused by several species of *Banana streak virus*, which all produce typical leaf streak symptoms that can become necrotic (Fig. I-11A). More severe symptoms can be observed including pseudostem splitting (Fig. I-11B), necrosis of the leaf cigar, bunch constriction and internal necrosis and emerging of the flower bud and bunch from the side of pseudostem (Fig-11C). Internal and external necrosis symptoms can also be observed on fruits (Fig. I-11D).

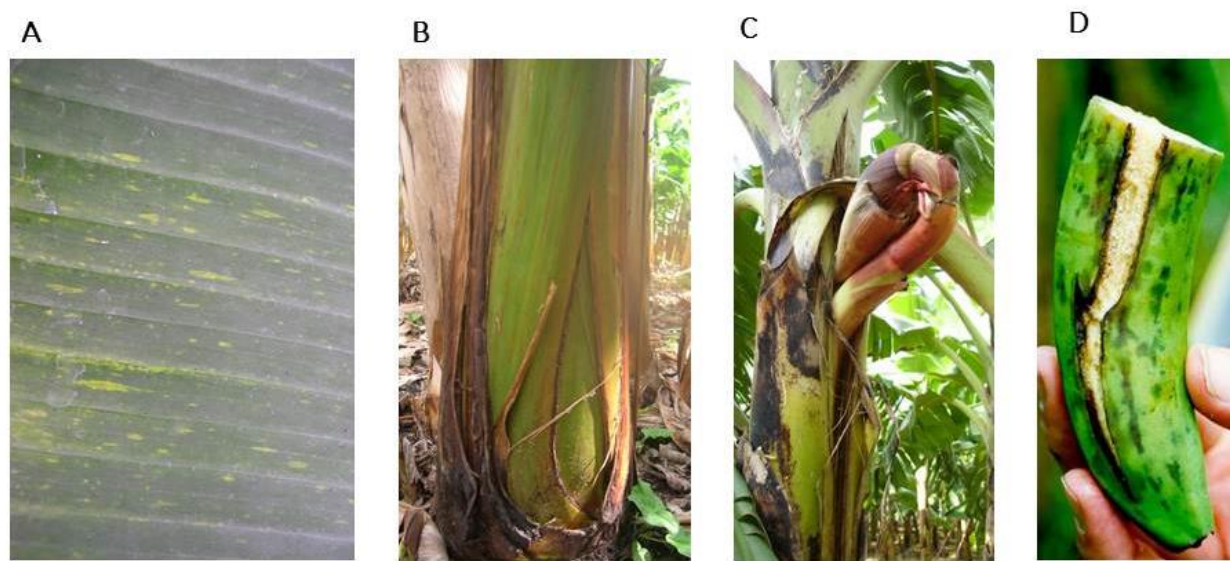


Figure I-11: BSV symptoms on leaf (A), pseudostem (B), flower bud (C) and fruit (D)

Sources: A, B, C: P.-Y. Teycheney © CIRAD; D: S. Dallot © CIRAD

Environmental conditions such as temperature and water stress influence symptomatology (Dahal *et al.*, 1998a; Gauhl *et al.*, 1999; Lockhart & Jones, 2000) and might explain why intermittent symptoms are often observed (Lockhart & Jones, 1999b; Dahal *et al.*, 2000). For example water deficiency can increase symptoms (Hughes, 1998), but increased symptoms have also been reported during rainy season (Ortiz, 1996; Dahal *et al.*, 1998a).

BSVs are present worldwide, in all banana production areas (Fargette *et al.*, 2006; Lockhart & Jones, 2000). Impact of viral infections on plant production is poorly documented, including that of BSVs on banana production. Measuring the impact of BSCAV infection on the growth and yield of dessert banana cultivar Williams in northern Queensland (Australia), Daniells *et al.* (2001) reported that it is limited, although it seems to increase in ratoon crops. Maximum yield losses were 11% per annum, resulting from an extended delay of 9 days between the harvest of plant and ratoon crops. Limited impact on production was also reported in Africa in plantain and banana (Dahal *et al.*, 1998). Serious local outbreaks are reported on a regular basis in Latin America and Africa (Geering, *et al.*, 2009; Baranwal *et al.*, 2014), especially on dessert banana. Although they never seem to spread to large areas, they can cause important yield losses locally (Harper *et al.*, 2005).

I-3.5.2. Taxonomy, genome organization and molecular diversity

Banana streak viruses are members of the genus *Badnavirus*, family *Caulimoviridae* (<http://www.ictvonline.org/virusTaxonomy.asp>). The family *Caulimoviridae* is the only family of dsDNA viruses in the plant kingdom. It includes seven additional recognized genera (*Caulimovirus*, *Cavemovirus*, *Petuvirus*, *Rosadnavirus*, *Solendovirus*, *Soymovirus* and *Tungrovirus*). All viruses of this family have a circular dsDNA genome with one discontinuity on one strand and one or more on the other that are associated with the replication process. They are DNA reverse-transcribing viruses (or pararetroviruses), meaning that their replication cycle contains a reverse transcription step that uses a more than genome length transcript as a template. Another common feature of *Caulimoviridae* is that all the coding information is on one strand of the genome.

BSVs and other badnaviruses have non-enveloped, bacilliform viral particles approximately 30 × 150 nm in size (Fig. I-11A) containing one copy the dsDNA circular genome of 7–8 kbp (Fig. I-11B). This genome contains three open reading frames. ORF I and ORF II potentially encode two proteins of respectively ca 20 kDa and ca 14 kDa, whose functions remain unknown. However, a role in virus assembly has been suggested for homologous proteins of other members of the family *Caulimoviridae* (Jacquot *et al.*, 1996; Stavelone *et al.*, 2001). ORF III encodes a large polyprotein of ca 210 kDa with conserved domains associated to cell-to-cell movement, coat protein and replicase functions (aspartic protease, reverse transcriptase and RNase H1; Geering *et al.*, 2011). The aspartic protease would cleave the polyprotein into functional proteins.

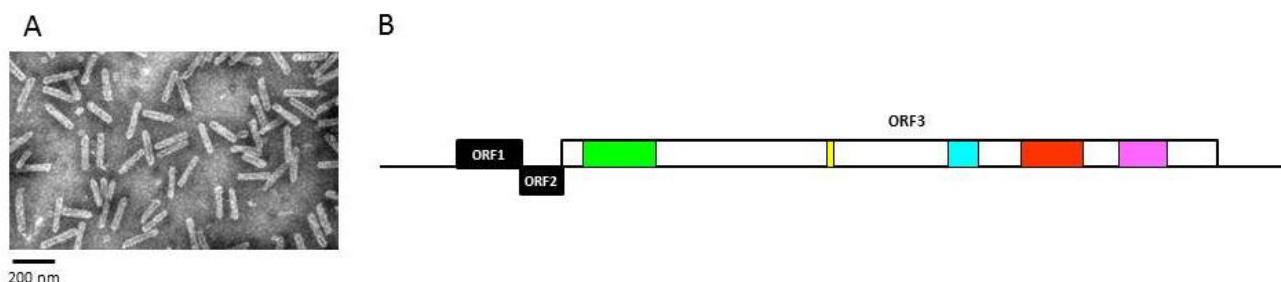


Figure I-12: Viral particles and genome organization of *Banana streak virus*

A: Purified viral particles of BSMYV (© J. Vo, the University of Queensland)

B: Linearized genome map of *Banana streak IM virus*. Colored regions within ORF3 are conserved protein domains as listed in the Pfam database (<http://pfam.sanger.ac.uk/>). Green: viral movement protein domain (PF01107), corresponding to L43–E243 of the cauliflower mosaic virus (CaMV) ORF1 protein; light blue: retro pepsin (pepsin-like aspartic protease) domain (CD00303), corresponding to K36–Q120 of the CaMV ORF5 protein; red: reverse transcriptase domain (CD01647), corresponding to K273–G449 of the CaMV ORF5 protein; purple: RNase H1 domain (CD06222), corresponding to I547–E673 of the CaMV ORF5 protein; yellow: zinc finger. Adapted from Geering *et al.* (2011).

So far, nine species of *Banana streak virus* (BSV) have been recognized by the International Committee for the Taxonomy of Viruses (ICTV) although the genomes of more species have been fully sequenced (Table I-10).

Table I-4: *Banana streak virus* species for which full genome sequences are available

Acronym	Name	Reference
BSVNV*	Banana streak Vietnam virus	Lheureux <i>et al.</i> , 2007
BSAcYunV	Banana streak acuminata Yunnan virus	Zhuang <i>et al.</i> , 2011
BSGFV*	<i>Banana streak Goldfinger virus</i>	unpublished
BSIMV*	<i>Banana streak Imové virus</i>	Geering <i>et al.</i> , 2014
BSMYV*	<i>Banana streak Mysore virus</i>	Geering <i>et al.</i> , 2005
BSOLV*	<i>Banana streak Obino l'Ewai virus</i>	Harper & Hull, 1998
BSUAV*	<i>Banana streak UA virus</i>	James <i>et al.</i> , 2011
BSUIV*	<i>Banana streak UI virus</i>	
BSULV*	<i>Banana streak UL virus</i>	
BSUMV*	<i>Banana streak UM virus</i>	
BSCAV	Banana streak CA virus	

* : species recognized by the International Committee for the Taxonomy of Viruses

Phylogenetic analyses performed on full-length genome sequences of BSVs and other badnaviruses representative of the diversity of the genus showed that BSVs display a high level of diversity (Fig. I-12). Based on the species delineation criteria recognized by the ICTV (a 20% difference between two nucleotidic sequences), all fully sequenced BSV genomes belong to distinct species. This illustrates the very high level of molecular diversity among BSVs.

Phylogenetic studies also show that BSV species are distributed over two of the three clades structuring the genus badnavirus (Harper *et al.*, 2005): clade 1, which includes BSV species collected worldwide, and clade 3, which contains only BSV species from Uganda (Iskra-Caruana *et al.*, 2014). BSV species are closer to badnaviruses infecting other host plants than from other BSVs. This is especially true of BSOLV, BSCAV and BSUAV, which are closer to Sugarcane bacilliform Guadeloupe A virus than from any other BSV, and for BSMYV, which is closer from SCBV, isolate 3D than from any other BSV (Fig. I-12).

This finding supports the hypothesis that BSVs may have evolved from *Sugarcane bacilliform virus* (SCBV) following a host shift from sugarcane to banana (Muller *et al.*, 2011; Iskra-Caruana *et al.*, 2014). This hypothesis is also supported by the fact that SCBV can be experimentally transmitted to banana (Bouhida *et al.*, 1993) and that inter BSV-SCBV recombination events took place, most probably during the infection of a common host before host shift (Sharma *et al.*, 2015).

I-3.5.3. Transmission

Transmission of BSVs is mediated by at least six of the nineteen species of mealybugs (family *Pseudococcidae*) known to occur on banana: *Planococcus citri*, *P. ficus*, *P. minor*, *Dysmicoccus brevipes*, *Paracoccus burnerae* and *Saccharicoccus sacchari* (Lockhart & Olszewski, 1993 ; González Arias *et al.*, 2002; Meyer *et al.*, 2008; Muturi *et al.*, 2013). Mealybugs colonize the underside of banana leaves, bunches, flowers and feed on plant sap by forcing their needle-like piercing mouthparts into the plant. BSV transmission by mealybugs occurs under the semi persistent mode: the virus gets into the vector's digestive track but does not multiply in the vector. It is regurgitated during feeding process and injected into plant sap. Field observations suggest that mealybug transmission of BSV is not very efficient and does not play a significant role in BSV epidemiology (Fargette *et al.*, 2006), because mealybugs do not move very much. However, they can be moved from plant to plant by ants (Jones, 2000), which develop symbiotic relationships with mealybugs, feeding on mealybugs honeydew and protecting them from their natural predators. Therefore, BSV control measures include the control of mealybugs and ants by insecticide treatment. It is interesting to note that *S. sacchari* can also transmit SCBV to banana (Lockhart & Autrey, 1991), and could therefore have played a role in the hypothesized host shift of SCBV from sugarcane to banana (see above).

A more unique (vertical) transmission mode concerns several species of BSV (BSOLV, BSGFV and BSIMV). It is based on the activation of endogenous viral elements of BSV called endogenous BSV sequences (eBSVs) that are present in the genome of all known *M. balbisiana* genotypes (see below; Ndowora *et al.*, 1999; Harper *et al.*, 1999; Dallot *et al.*, 2000; Geering *et al.*, 2001; Gayral *et al.*, 2010; Duroy *et al.*, 2015)

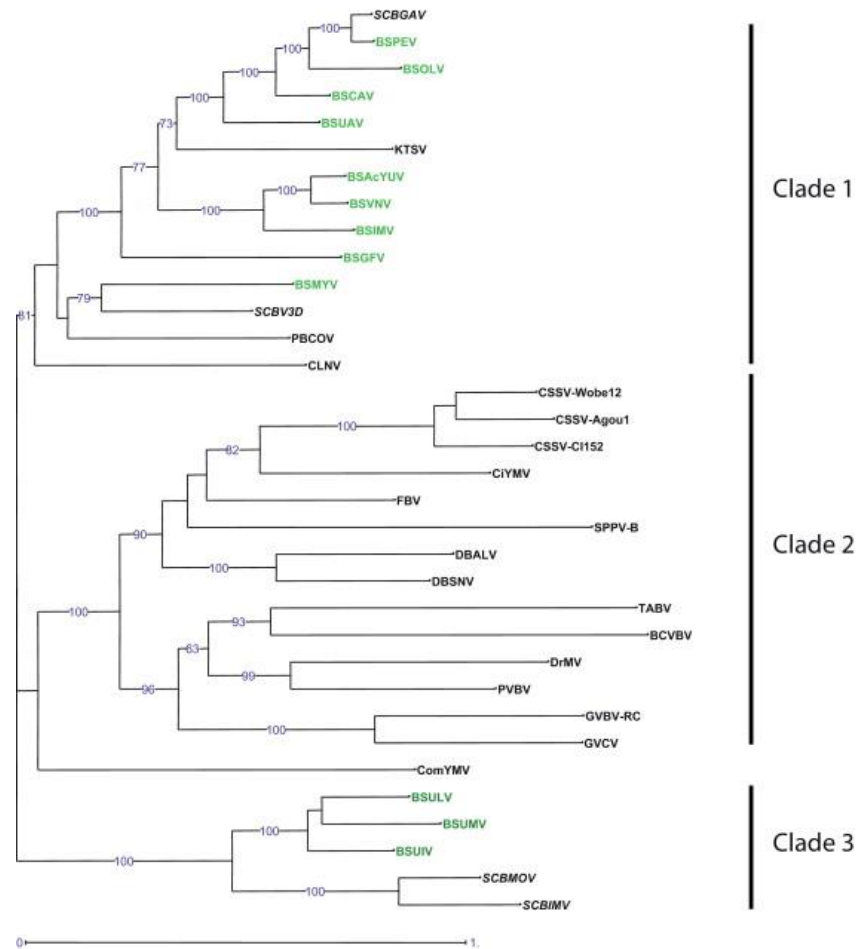


Figure I-13: Maximum likelihood phylogeny of badnavirus sequences established with the alignment of full-length viral genome sequences.

Bootstrap values of 500 replicates are given when >60%. The scale bar shows the number of substitution per base. List of viruses and their acronyms is as follows: *Banana streak OL virus*, BSOLV; *Banana streak MY virus*, BSMYV; *Banana streak acuminata Vietnam virus*, BSVNV; *Banana streak GF virus*, BSGFV; *Banana streak IM virus* (BSIMV); *Banana streak CA virus* (BSCAV); *Banana streak Uganda A virus* (BSUAV); *Banana streak Uganda I virus* (BSUIV); *Banana streak Uganda L virus* (BSULV); *Banana streak Uganda M virus* (BSUMV); *Banana streak acuminata Yunnan virus* (BSAcYUV); *Banana streak Peru virus* (BSPEV); *Bougainvilleae spectabilis chlorotic vein-banding virus*, (BCVBV); *Cacao swollen shoot virus Agou1 isolate* (CSSV-Agou1-); *Cacao swollen shoot virus CI152 isolate* (CSSV-CI152); *Cacao swollen shoot virus Wobe 12 isolate* (CSSV-Wobe12); *Commelina yellow mottle virus* (ComYMV); *Citrus yellow mosaic virus* (CiYMV); *Cycad leaf necrosis virus* (CLNV); *Dioscorea bacilliform AL virus* (DBALV); *Dioscorea bacilliform SN virus* (DBSNV); *Dracaena mottle virus* (DrMV); *Fig badnavirus* (FBV); *Gooseberry vein banding virus RC isolate* (GVBV-RC); *Grapevine vein clearing virus* (GVCV); *Kalanchoe top-spotting virus* (KTSV); *Pelargonium vein banding virus* (PVBV); *Pineapple bacilliform comosus virus* (PBCoV); *Sugarcane bacilliform MO virus* (SCBMOV); *Sugarcane bacilliform IM virus* (SCBIMV); *Sugarcane bacilliform Guadeloupe A virus* (SCBGAV); *Sugarcane bacilliform Guadeloupe D virus* (SCBGDV); *Sweet potato pakakuy B virus* (SPPV-B); *Taro bacilliform virus* (TABV). BSV genomes are in green, SCBV genomes in italics.

From Iskra-Caruana et al. (2014).

I-4. Breeding improved banana varieties

I-4.1. Conventional breeding

Considering the importance of banana for the economy and food security worldwide, breeding improved varieties has been a priority for almost a century. The first conventional breeding programs were established in Trinidad and Jamaica in the 1920's, aiming at introgressing resistance traits against *Fusarium* wilt, a devastating fungal disease also known as Panama disease (see IV-2), into the then worldwide dominant AAA triploid dessert cultivar grown for export, Gros Michel. Despite its many qualities, including the production of remarkably tasty fruits with extended shelf life that make them ideal for export, this cultivar is highly sensitive to *Fusarium* wilt. Because they are parthenocarpic, hence seedless, edible banana –including Gros Michel– are clonally (vegetatively) propagated. Therefore, large scale cultivation of Gros Michel clonal and uniform populations offered *Fusarium oxysporum*, the causal agent of the Panama disease, an ideal ground to spread around the world. And it did: by the end of the 1950's, Gros Michel had been wiped out, forcing an unprecedented worldwide shift to another AAA triploid variety called Cavendish, which is less tasty but is resistant to Panama disease. This sad example is one among many that illustrate the never-ending biological arms race between plants and pests, and the need to improve crops to help them resist to emerging diseases. It also illustrates the difficulty to breed new banana varieties.

As mentioned above, edible bananas are highly sterile. This ensures that they do not produce seeds that would make them impossible to commercialize. Unfortunately, it also results in an extremely low residual fertility that renders breeding almost impossible: amazingly high numbers of hand pollinations are required to obtain a handful of seeds that do not germinate spontaneously and contain very often non-viable embryos, because they are either aneuploid (missing one or more chromosomes) or hyperploids (having more than 4 copies of each chromosome). This is especially true of dessert AAA triploid cultivars such as Gros Michel and Cavendish. Furthermore, triploid banana cultivars probably arose from a very limited number of meiosis events (20 to 25), resulting in a narrow genetic basis that makes them fragile.

To overcome these difficulties, banana breeders have developed two complementary strategies, using wild (and fertile) *M. acuminata* and *M. balbisiana* seedy progenitors (Bakry *et al.*, 1990; Bakry *et al.*, 2001; Tomekpe *et al.*, 2004):

- A 4x/2x strategy aiming at producing improved triploid dessert bananas from wild fertile diploid parents. One of the parents is made tetraploid following colchicine treatment, which results in chromosome doubling (Bakry *et al.*, 2009).
- A 3x/2x strategy aims at producing improved triploids for local markets. It relies on the production of improved diploids with traits introduced from wild sources in an improved genetic background. These improved diploids are then used as male parents in crosses with the desired triploid as female parent. However, this strategy suffers from the low fertility rate of triploid female parents.

Regardless of the chosen strategy, a key issue is the characterization of the traits of interest in the parents used in breeding schemes. In this regard, recent access to the complete sequences of the *M. acuminata* and *M. balbisiana* genomes (d'Hont *et al.*, 2012; Davey *et al.*, 2013), and to reference saturated physical maps (Hippolyte *et al.*, 2010) now allow the development of molecular markers, that are instrumental to marker-

assisted breeding and to the identification of the diploid progenitors that are best suited for breeding (Hippolyte *et al.*, 2012).

Breeding for pest and disease resistance is currently the priority of most conventional breeding programs, in order to alleviate the use of pesticides that is both costly and hazardous for the environment and for public health. Despite undisputable success in developing hybrid varieties with resistance against Black Sigatoka (Abadie *et al.*, 2009) or tolerance to nematodes or weevils, conventional breeding has not yet delivered hybrids with resistance against other major diseases such as *F. oxysporum* tropical race 4, which is the most serious threat to banana cultivation worldwide. However, progress seems to be made in the identification of sources of resistance that could be used for breeding purposes (Khayat *et al.*, 2009). Moreover, there is hope that mass screening combined with genomic approaches will allow the identification of more sources of resistance that could be used for breeding purposes as well.

Other traits of interests sought by breeders include decreased plant height (with dwarfism being a much sought character as dwarf plants are easier to harvest), yield, bunch weight, fruit filling time, fruit length and leaf number.

There are still relatively few banana breeding programs worldwide considering the importance of the crop. However, their number has increased over the last 20 years. The main breeding programs are based in Africa, (Centre Africain de Recherches sur Bananiers et Plantain (CARBAP) in Cameroon; Centre National de Recherche Agronomique (CNRA) in Côte d'Ivoire; International Institute of Tropical Agriculture (IITA) in Nigeria and Uganda; National Agricultural Research Organisation (NARO) in Uganda), in Asia (Chinese Academy of Tropical Agricultural Sciences (CATAS) and Guangdong Academy of Agricultural Sciences (GDASS) in China; Indonesian Fruits Research Institute (ITFRI) in Indonesia; National Research Centre for Banana (NRCB) in India and in the Americas (Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD) in Guadeloupe; Empresa Brasileira de Pesquisa Agropecuária (Embrapa) in Brazil; Fundación Hondureña de Investigación Agrícola (FHIA) in Honduras).

I-4.2. Non-conventional breeding

The progress made in molecular biology and tissue culture in the 1970's and 1980's paved the way to genetic transformation, eventually leading to the first transgenic plants (Fraley *et al.*, 1983). From then on, plant biotechnology emerged as a very active and productive domain. However, several important crops, mostly monocotyledonous plants amongst which cereals and banana, remained recalcitrant to transformation for a long time and it took additional innovations to achieve transformation of banana both by *Agrobacterium* (May *et al.*, 1995) and by direct bombardment of embryogenic suspension cells (Sági *et al.*, 1995).

Besides the much publicized transgenic banana with increased micronutrient content, including pro vitamin A, genetic engineering of banana has surprisingly achieved little, considering the amount of funding that it has attracted. There are, however, two noticeable and major achievements. Firstly, transgenic banana (*Musa acuminata* 'Gros Michel') expressing chitinase genes were obtained and shown to express resistance against Black Sigatoka (Kovács *et al.*, 2013). Secondly, transgenic dessert banana cultivar Rasthali (AAB, Silk group) expressing small interfering RNAs (siRNAs) targeting the master replication initiation protein (Rep) of Banana bunchy top nanovirus (BBTV) were obtained and some transgenic lines were shown to be completely resistant to BBTV infection (Shekhawat *et al.*, 2012). However, no data from field testing of these transgenic lines is

currently available, contrary to Black Sigatoka-resistant hybrids which have been positively evaluated under field conditions e.g. Therefore it is not yet possible to evaluate the efficiency of these transgenic lines and their usefulness for farmers.

Moreover, considering the reject of genetically modified (GM) crops by the public opinion in most countries, especially in developed countries that are the main export markets for banana producers, adoption of disease-resistant GM banana seems less than likely, at least in the near future.

I-4.3. Hybrid varieties cultivated in the Dominican Republic

Besides the traditional cultivars grown in the Dominican Republic (see II-2), four hybrids are cultivated, sometime to a large extent (FHIA-03, FHIA-18, FHIA-21 and FHIA-25, see II-2). All four of them were obtained by the FHIA breeding program and are resistant to Black Sigatoka, with FHIA-21 and FHIA-25 displaying the highest resistance levels. These hybrids were introduced in the country in 1994 in anticipation of the introduction of Black Sigatoka, which was progressing swiftly in all neighboring countries (Cuba, Jamaica and Venezuela). The disease finally hit the Dominican Republic in 1996.

Since FHIA-21 is the only hybrid used in this study, we will detail its main characteristics.

FHIA-21 is a French type plantain hybrid that was created in 1987 from a cross between an AAB plantain of the French group, cv. AVP-67, and a diploid AA parent (SH-3142). It displays high resistance levels against Black Sigatoka and Panama disease but is sensitive to nematodes *Radopholus similis* and *Pratylenchus coffeae* (Carranza, *et al.*, 2011).

Plants are 3.5 to 4 meters high and produce bunches of average weight of 20-30 kg containing 65-80 large fingers weighing 250-350 grams each. It is considered a high yield plantain compared to other types such as False Horn. Fruits have a short shelf life, but it can be increased with proper harvesting by age and calibration. Despite a tendency to bruise, fruits have excellent processing qualities. Hence, FHIA-21 is extremely successful in the banana chips industry and it is estimated that it occupies 43% of the total area planted in plantain in the Dominican Republic (Espinosa, 2011). However, being an interspecific hybrid, FHIA-21 harbors the *M. balbisiana* genome, which contains copies of infectious endogenous BSVs (eBSVs) whose activation by abiotic stresses leads to spontaneous infections by cognate BSV species (see below, I-5-3).

I-5. Endogenous viral elements (EVEs)

I-5.1. What are endogenous viral elements and how did they get there?

Endogenous viral elements (EVEs) are viral sequences that have been integrated into the genomes of their hosts through active or passive horizontal gene transfer (HGT). In multicellular eukaryotes, EVEs can be transmitted to progenies following their integration in germ-line nuclei (Feschotte & Gilbert, 2012).

Active HGT involves enzymes called integrases that are encoded by the genome of viruses such as retroviruses e.g: in their case, integration is an obligatory step in the replication cycle. The integrated form (called provirus) is passed to the offspring when infection occurs in germline cells. The term endogenous has been coined to distinguish such vertical transmission from horizontal transmission between individuals following more

conventional infection pathways. Once fixed in the host genetic lineage, endogenous retroviruses evolve like a pseudogene: they accumulate mutations and progressively lose their infectivity. In plants, long terminal repeat (LTR)-retrotransposons, also called class I transposable elements, are closely related to retroviruses and share many features with them, including common gene functions and replication strategy. They do produce virus-like particles and are considered viruses by the ICTV. They are classified into two families: *Metaviridae* (gypsy-like retrotransposons) and *Pseudoviridae* (copia-like retrotransposons) (Fauquet *et al.*, 2005).

Access to complete genome sequences unveiled the presence of non-retroviral EVEs in the genome of mammals, insects and plants (Bézier *et al.*, 2009; Delaroque & Boland, 2008; Frank & Wolfe, 2009; Staginnus & Richert-Pöggeler, 2006; Werren *et al.*, 2010; Chiba *et al.*, 2011). In the case of non-retroviral EVEs, integration is not an active process because cognate viruses do not encode an integrase. Integration occurs through non-homologous end-joining (also called illegitimate recombination) during repairs of dsDNA breakages (Puchta, 2005). Any type of DNA with minimal homology with acceptor DNA molecules can be used as repair material to fill in the gaps, including DNA of viral origin. Molecular studies showed that non retroviral EVEs abound in the genomes of insects, mammals and plants, including sequences from viruses with RNA genomes (Crochu *et al.*, 2004; Horie *et al.*, 2010; Geuking *et al.*, 2009; Teycheney & Geering, 2011).

I-5.2. Plant EVEs

In plants, most known EVEs originate from viruses with DNA genomes in the families *Caulimoviridae* and *Geminiviridae* (Teycheney & Geering, 2011; Hohn *et al.*, 2008; table I-5). Viruses in these families do not encode an integrase, therefore corresponding EVEs were integrated by non-homologous end-joining.

Endogenous *Geminiviridae* sequences were the first plant EVEs to be characterized in the genome of several *Nicotiana* species (Kenton *et al.*, 1995; Bejarano *et al.*, 1996; Ashby *et al.*, 1997; Murad *et al.*, 2004). They were called *Geminivirus*-related DNA (GRD) and classified into three groups depending on copy number and *Nicotiana* host species. Interestingly, they all contain a truncated begomoviral rep gene and a fragment of begomoviral intergenic region including an origin of replication-like sequence. GRDs are essentially ‘fossil records’ (Katzourakis 2013). They are too fragmented and too degenerated to be replication competent and are likely to be non-infectious. More recently, *in silico* analyses showed that the genomes of lettuce (*Lactuca sativa*), apple (*Malus x domestica*), coffee (*Coffea canephora*) and poplar (*Populus trichocarpa*) also host GRDs (Liu *et al.* 2011; Martin *et al.*, 2011). Filloux *et al.* (2015) reported two new classes of geminivirus-like elements (EGV1 and EGV2) in the genome of yams (*Dioscorea* spp. of the *Enantiophyllum* clade).

Historically, the first described EPRVs were endogenous *Banana streak virus* sequences (eBSVs) that were discovered in *Musa* genomes by Southern blot (Lafleur *et al.*, 1996). Soon after, spontaneous viral infections in petunia, tobacco and banana by *Petunia vein clearing virus* (PVCV), respectively *Tobacco vein clearing virus* (TVCV) and *Banana streak virus* (BSV), were observed following stress, wounding or tissue culture (Dallot *et al.*, 2001; Harper *et al.*, 1999; Lockhart *et al.*, 2000; Ndowora *et al.*, 1999; Richert-Pöggeler & Shepherd, 1997; Richert-Pöggeler *et al.*, 2003). These observations lead to the finding that some endogenous forms of these viruses are infectious. Numerous EPRVs were characterized by standard molecular techniques such as PCR and Southern blot, prompting efforts to organize their classification under the rules enforced by the ICTV (Geering *et al.*, 2010). More recently, the access to complete plant genome sequences unveiled the extent of the invasion of plant genomes by *Caulimoviridae* sequences. Recent systematic searches for such sequences lead to the

discovery of a completely new genus within the family *Caulimoviridae*, tentatively named Florendovirus (Geering *et al.*, 2014). A total of 34 complete or near complete genomes of distinct novel viral species were assembled from genomes of a wide range of angiosperms, showing that florendoviruses literally invaded the genome of flowering plants and contribute significantly to many of these genomes (Table I-6). Although several endogenous florendoviruses could potentially be replication competent and therefore infectious, there is no evidence that cognate viruses are still extant; on the contrary, evidence suggests that the genus is entirely fossile.

The conservation of EVEs throughout the plant evolution raises questions about their possible roles in plant biology and this issue is being increasingly investigated. Mushegian & Elena (2015) recently reported on the ubiquitousness of functional *Caulimoviridae*-related sequences encoding homologs of the *Tobacco mosaic virus* 30K movement protein in the genomes of ferns, gymnosperms and angiosperms. They showed that these viral genes underwent positive selection and are transcribed in mRNAs. Authors suggest that they could play a role in the control of organ differentiation in higher plants. Filloux *et al.* (2015) showed that two endogenous geminivirus-like elements (EGV1 and EGV2) are present in the *Dioscorea* spp. of the Enantiophyllum clade. Interestingly, these authors showed also the presence of EGV gene transcripts, small 21–24 nt RNAs that are apparently derived from these transcripts and provided experimental evidence showing that EGV-encoded Rep proteins are expressed in *D. alata*. These data suggest that EGV genes are functionally expressed in *D. alata* and raise questions about possible beneficial roles of these EGV for their host plants. These pioneering data suggest that capture of beneficial genes from viruses might have occurred in plants like they have in mammals (Dupressoir *et al.*, 2009). It has also been hypothesized that plant EVEs could play a role in defending against infection by cognate exogenous viruses, by acting as natural viral transgenes and triggering silencing-based mechanisms (Bertsch *et al.*, 2009; Hansen *et al.*, 2005; Koonin, 2010; Mette *et al.*, 2002; Noreen *et al.*, 2007; Teycheney & Tepfer, 2007).

The presence in plants of 21-24nt small interfering RNAs homologous to both EVEs and cognate viruses (Geering *et al.*, 2014), which are hallmarks of silencing-based antiviral defense mechanisms, supports this hypothesis. However, a formal demonstration is still missing. EVEs might also contribute to plant evolution by acting on gene regulation mechanisms. Viral promoters present in EVEs could upregulate plant genes; on the contrary, random insertion of EVEs could disrupt plant genes and lead to phenotypic changes such as somaclonal variants (Geering *et al.*, 2004). Integration of EVEs in plant genomes could also contribute, like transposable elements, to the variation in the size of plant genomes, which plays a key role in plant adaptation to environmental changes (Hawkins *et al.*, 2009).

Table I-5: Plant endogenous viral elements

Host plant	Endogenous viral element					References
	Complete viral genome	Infectious	Acronym	Viral family	Viral genus	
Banana (<i>Musa balbisiana</i>)	yes	yes	eBSOLV*, eBSGFV*, eBSImV*, eBSMysV	Caulimoviridae	Badnavirus	Chabannes <i>et al.</i> , 2013; Gayral <i>et al</i> 2008 ; Gering <i>et al.</i> (2005b).
Banana (<i>Musa balbisiana</i>)	no	no	BEV9, BEV11, BEV14, BEV15, BEV20, BEV21, BEV23, BEV25, BEV26, BEV27	Caulimoviridae	Badnavirus	Geering <i>et al</i> 2005a
Banana (<i>M. acuminata</i> x <i>M. balbisiana</i> hybrids)	no	no	BEV16, BEV17, BEV18, BEV19, BEV22, BEV28, BEV29, BEV30, BEV33	Caulimoviridae	Badnavirus	Geering <i>et al</i> 2005a
Banana (<i>Musa schizocarpa</i>)	no	no	BEV10, BEV13	Caulimoviridae	Badnavirus	Geering <i>et al</i> 2005a
Yam (<i>Dioscorea rotundata</i>)	NK	NK	eDBV	Caulimoviridae	Badnavirus	Umber <i>et al.</i> , 2014
Dahlia (<i>Dahlia mirabilis</i>)	NK	NK	eDMV-D10	Caulimoviridae	Caulimovirus	Pahalawatta <i>et al.</i> 2008
Trifoliolate orange (<i>Poncirus trifoliata</i>)	NK	NK	ND	Caulimoviridae	Caulimovirus	Yang <i>et al.</i> 2003a
Angiosperms	yes	NK	34 distinct species	Caulimoviridae	Florendovirus	Geering <i>et al.</i> , 2014
Rice (<i>Oryza sativa</i>)	yes	NK	eOsatV-A, eOsatV-B, eOsatV-C	Caulimoviridae	Orendavirus	Kunii <i>et al.</i> 2004; Geering <i>et al.</i> 2010
Petunia (<i>Petunia hybrida</i>)	yes	yes	ePVCV*	Caulimoviridae	Petuvirus	Richert Pöggeler <i>et al.</i> 2003
Potato (<i>Solanum tuberosum</i>)	NK	NK	Sotul, SotulII	Caulimoviridae	Solendovirus	Hansen <i>et al.</i> 2005
Tobacco (<i>Nicotiana edwardsonii</i>)	yes	yes	eTVCV*	Caulimoviridae	Solendovirus	Lockhart <i>et al.</i> 2000; Geering <i>et al.</i> 2010
Tobacco (<i>Nicotiana glauca</i> , <i>N. glauca</i> sp.)	NK	NK	eTVCV	Caulimoviridae	Solendovirus	Jakowitsch <i>et al.</i> 1997; Geering <i>et al.</i> 2010
Tobacco (<i>Nicotiana tomentosiformis</i> , <i>N. tomentosiformis</i> , <i>Nicotiana</i> sp.)	NK	NK	eTVCV	Caulimoviridae	Solendovirus	Gregor <i>et al.</i> 2004; Geering <i>et al.</i> 2010
Tomato (<i>Solanum lycopersicum</i>)	NK	NK	eTVCV	Caulimoviridae	Solendovirus	Staginnus <i>et al.</i> 2007; Geering <i>et al.</i> 2010
Grape (<i>Vitis vinifera</i>)	NK	NK	ND	Caulimoviridae	Unassigned	Bertsch <i>et al</i> 2009
Pineapple (<i>Ananas comosus</i>)	NK	NK	AcEV	Caulimoviridae	Unassigned	Gambley <i>et al.</i> 2008
Poplar (<i>Populus trichocarpa</i>)	yes	NK	ND	Caulimoviridae	Unassigned	Bertsch <i>et al</i> 2009
Tobacco (<i>Nicotiana kawakamii</i> , <i>N. tomentosa</i> , <i>Nicotiana tomentosiformis</i>)	no	no	GRD2, GRD3, GRD5	Geminiviridae	Begomovirus	Kenton <i>et al.</i> , 1995; Bejarano <i>et al.</i> , 1996; Ashby, <i>et al.</i> , 1997; Murad <i>et al.</i> , 2004
Yam (<i>Dioscorea</i> spp)	no	NK	EGV1, EGV2	Geminiviridae	Begomovirus	Filloux <i>et al.</i> , 2015

*: Infectious EVE

Updated from Teycheney & Geering (2011)

Table I-6. Contribution of endogenous florendoviruses to the genomes of various plant species.

Species	Plant genome assembly size (bp)	Endogenous florendovirus elements coverage (bp)	Genome fraction made of endogenous florendovirus elements (in %)
<i>Amborella trichopoda</i>	668,257,121	5,674,476	0.85
<i>Aquilegia caerulea</i>	301,982,859	242	0.00
<i>Arabidopsis lyrata</i>	206,667,935	36,979	0.02
<i>Arabidopsis thaliana</i>	119,146,348	3,438	0.00
<i>Brachypodium distachyon</i>	271,923,306	0	0.00
<i>Carica papaya</i>	342,680,090	0	0.00
<i>Chlamydomonas reinhardtii</i>	120,404,952	0	0.00
<i>Citrus clementina</i>	295,550,349	2,003,650	0.68
<i>Citrus sinensis</i>	319,231,331	1,272,462	0.40
<i>Cucumis sativus</i>	203,058,019	335,781	0.17
<i>Eucalyptus grandis</i>	691,297,852	797,465	0.12
<i>Fragaria vesca</i>	214,219,504	339,506	0.16
<i>Glycine max</i>	973,344,380	1,889,571	0.19
<i>Gossypium raimondii</i>	763,818,933	757,990	0.10
<i>Jatropha curcas</i>	285,858,490	2,806,965	0.98
<i>Linum usitatissimum</i>	318,250,901	0	0.00
<i>Malus domestica</i>	881,278,625	1,016,000	0.12
<i>Manihot esculenta</i>	532,507,280	234,896	0.04
<i>Medicago truncatula</i>	307,481,907	219	0.00
<i>Mimulus guttatus</i>	321,726,589	68,534	0.02
<i>Oryza sativa</i>	373,706,981	123,914	0.03
<i>Panicum virga</i>	1,358,078,670	4,078	0.00
<i>Phaseolus vulgaris</i>	486,869,582	720	0.00
<i>Physcomitrella patens</i>	479,985,347	0	0.00
<i>Populus trichocarpa</i>	417,137,944	386,859	0.09
<i>Prunus persica</i>	227,252,106	530,315	0.23
<i>Ricinus communis</i>	350,631,014	4,662,131	1.33
<i>Selaginella moellendorffii</i>	212,761,159	0	0.00
<i>Setaria italica</i>	405,737,341	0	0.00
<i>Solanum lycopersicum</i>	781,666,411	300,953	0.04
<i>Solanum tuberosum</i>	727,424,546	305,991	0.04
<i>Sorghum bicolor</i>	738,540,932	48,368	0.01
<i>Theobroma cacao</i>	351,351,221	90,504	0.03
<i>Vitis vinifera</i>	486,198,630	3,152,021	0.65
<i>Zea mays</i>	2,065,722,704	0	0.00

From Geering et al., 2014.

I-5.3. Endogenous banana streak viruses (eBSVs)

Since the discovery of endogenous banana streak virus sequences (eBSVs), genetic and molecular studies have shown that eBSVs involved in BSV infections are present in the genome of *M. balbisiana* but not in that of *M. acuminata* (Lheureux et al., 2003; Gayral et al., 2010; D'Hont et al., 2012; Duroy et al., 2015) whereas eBSV-like sequences are present in that of cultivated banana genotypes of species *M. acuminata*, *M. balbisiana* and *M. schizocarpa* (Geering et al. 2001, 2005b; Gayral & Iskra Caruana, 2009; Iskra-Caruana et al., 2014). Evolutionary studies showed that although integration of BSV sequences is a recent and frequent phenomenon, eBSVs display an important diversity (Gayral & Iskra Caruana, 2009; Duroy, 2014). Most eBSVs seem to be harmless to their

host plant. However, in a limited number of cases, some eBSVs present in the *M. balbisiana* genome are infectious and lead to spontaneous infections in interspecific hybrids harboring the *M. acuminata* (A) et *M. balbisiana* (B) genomes, upon activation by abiotic stresses such as cell culture (Dallot *et al.*, 2001; Côte *et al.*, 2001). To date, only two other types of EPRVs have proved infectious: endogenous *Tobacco vein clearing virus* (eTVCV) in *Nicotiana edwardsonii*, which is an allohexaploid derived from a cross between *N. glutinosa* and *N. clevelandii*, and endogenous *Petunia vein clearing virus* (PVCV) in petunia hybrids *P. hybrida* resulting from a cross between *P. integrifolia* ssp. *inflata* and *P. axillaris* ssp. *Axillaris* (Lockhart *et al.*, 2000; Richert-Pöggeler *et al.*, 2003).

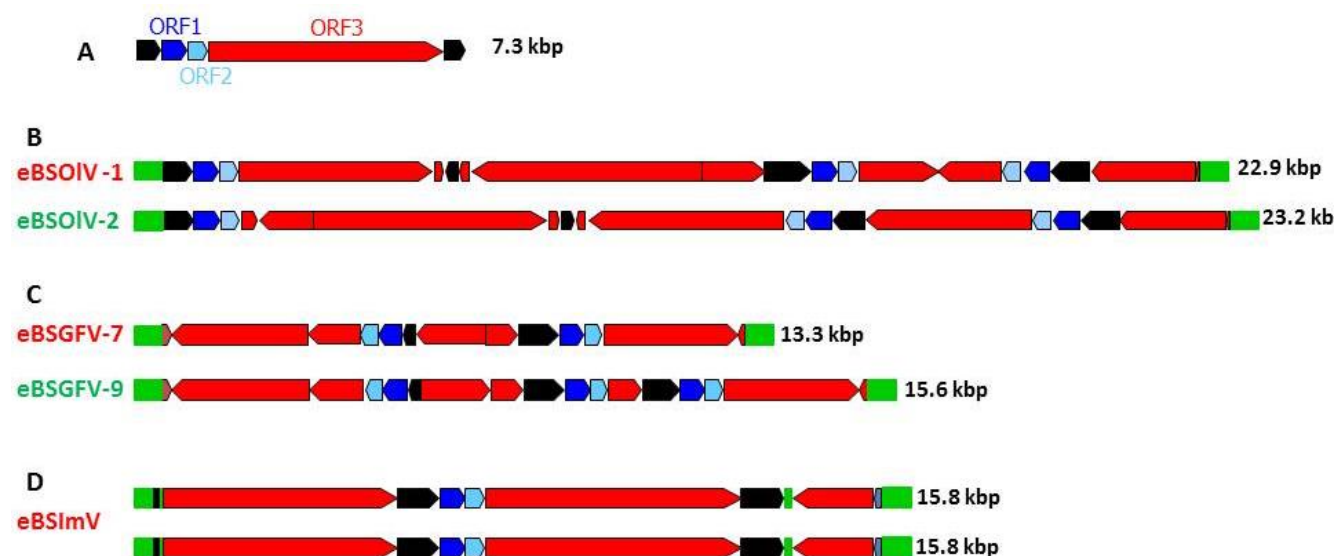


Figure I-14: Structure of eBSVs in PKW

A: linearized map of the BSV genome with ORF 1, ORF2 and ORF 3 represented respectively as dark blue, light blue and red boxes, and the intergenic region in black.

B, C, D: Structure of respectively eBSOLV, eBSGFV and eBSIMV, Infectious alleles (eBSOLV1, eBSGF7 and eBSIMV) are indicated in red and non-infectious alleles (eBSOL2, eBSGF9) in green.

Banana genomic sequences are represented as green boxes.

The size of viral genome and eBSVs is indicated.

From Chabannes *et al.* (2013), with modifications.

I-5.3.1 Structure of eBSVs

The fine molecular structure of eBSVs in the genome of the seedy *M. balbisiana* diploid model species Pisang Klutuk Wulung (PKW) was elucidated by Gayral *et al.*, 2008 and by Chabannes *et al.*, 2013. Their work showed that the genome of PKW harbours eBSVs for three distinct BSV species, namely BSOLV, BSGFV and BSIMV, that these eBSVs are highly rearranged and harbor numerous duplications when compared to the structure of corresponding viral genomes (Figure I-14). Genomic and cytological analyses by fluorescent in-situ hybridization (FISH) showed that each eBSV is present in the PKW genome at a single locus (Gayral *et al.*, 2008; Chabannes *et*

al., 2013), contrary to endogenous PVCV and TVCV which are scattered in very high copy numbers across the genomes of petunia and *N. edwardsonii*, respectively (Richert-Pöggeler *et al.*, 2003; Gregor *et al.*, 2004; Mette *et al.*, 2002). In PKW, eBSOLV and eBSGFV contain two distinct alleles of which one is infectious (eBSOLV1 and eBSGFV-7, respectively) whereas eBSIMV has two structurally identical alleles that are both infectious (fig I-14). A range of molecular markers derived from the structure of eBSVs was developed from the sequence of PKW eBSVs (Gayral *et al.*, 2008, 2010; Chabannes *et al.*, 2013). These markers are specific of either eBSV integration sites, structural features or allelic nature (infectious or non-infectious) (Figure I-15). These tools made it possible to genotype eBSVs in *Musa* spp and to show that all known *M. balbisiana* accessions conserved worldwide host at least one infectious eBSV (Duroy, 2014; Duroy *et al.*, 2015).

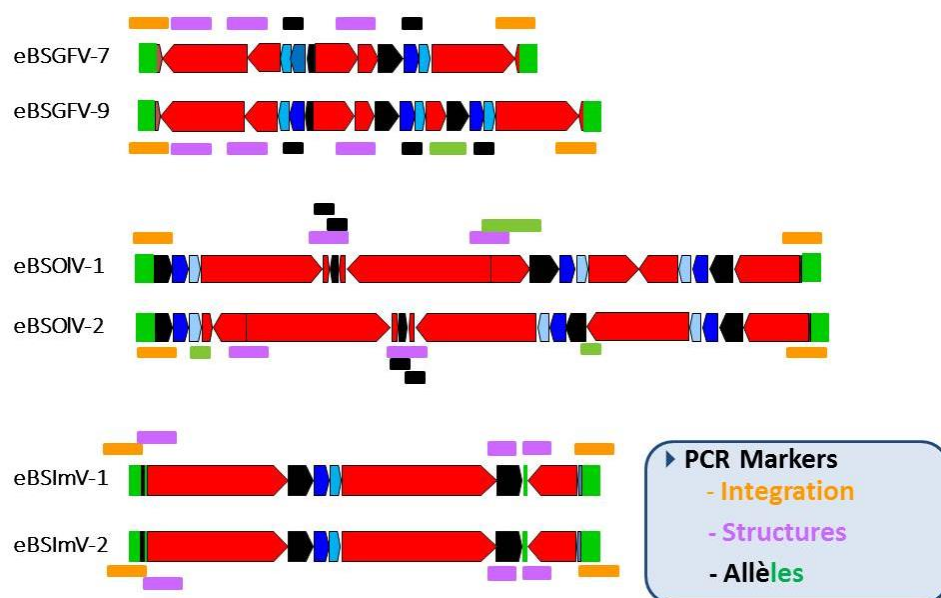


Figure I-15: Molecular markers used for genotyping eBSVs

The position of molecular eBSV-specific molecular markers is shown on the schematic map of the eBSVs characterized in PKW. Orange boxes figure markers specific of eBSV integration sites, purple boxes markers specific of the structure of eBSVs and black and green boxes allele-specific markers.

From Gayral *et al.* (2010), with modifications.

I-5.3.2 Activation of infectious eBSVs and its consequences on breeding, germplasm movement and multiplication

Infectious eBSV alleles give rise to episomal forms of cognate viruses upon activation by abiotic stresses such as cell culture. It is likely that abiotic stresses such as wounds and temperature differences can also activate the expression of infectious eBSVs, since they have been shown to do so for infectious endogenous forms of PVCV and TVCV (Lockhart *et al.*, 2000; Richert-Pöggeler *et al.*, 2003; Noreen *et al.*, 2007). Activation of infectious eBSVs occurs in interspecific hybrids of AAB and AAAB genotypes originating from natural hybridizations or genetic improvement programs altogether (Dallot *et al.*, 2001; Côte *et al.*, 2010). It has been hypothesized that the process requires the presence of an infectious allele as well as a genetic factor called BEL (BSV Expressed

Locus; Lheureux *et al.*, 2003). A model involving a double recombination event has been proposed to explain how functional BSGFV and eBSOLV genomes could be released from infectious eBSGFVs and eBSOLVs, respectively (Iskra-Caruana *et al.*, 2010; Chabannes & Iskra-Caruana, 2013).

The presence of infectious eBSVs in all available *Musa balbisiana* genetic resources is the main constraint for breeding new banana interspecific hybrids, due to the risk of large scale activation under field cultivation conditions, that could be amplified by vector (mealybug)-borne transmission (Meyer *et al.*, 2008), leading to BSV outbreaks. Although this risk has never been assessed, some genetic improvement programs, such as the one from CIRAD in Guadeloupe (French West Indies), have applied a strict precaution principle and banned the use of *M. balbisiana* genitors. They currently rely only on *M. acuminata* parents for breeding purposes. This hampers the introgression of traits of interest, such as drought tolerance, that could be brought by *M. balbisiana* parents. Infectious eBSVs are also an important constraint for the movement of *Musa* germplasm, in particular interspecific hybrids, due to the risk of introducing exotic BSV species through activatable infectious eBSVs. This has prompted international efforts to update the guidelines for exchanging *Musa* germplasm (Thomas, 2015). The risk of activation of infectious eBSVs in interspecific hybrids (Côte *et al.*, 2010) also prevents the use of cell culture for multiplying AAB plantains and other interspecific hybrids, despite an increasing demand resulting from the need to feed a human population in constant progression.

I-5.3.3 Impact of eBSVs on diagnosis

Symptom-based diagnosis of BSV is unreliable as symptomless infections occur frequently (Dahal *et al.*, 1998, 2000a) and BSV symptoms on leaves can be confused with CMV symptoms. Electron microscopy (ISEM) is very reliable but it is time consuming and requires sophisticated equipment. Serological detection by Enzyme Linked Immunosorbent Assay (ELISA) has shown a low sensitivity despite considerable time and effort put into the raising of a polyvalent antiserum (Lockhart & Olszewski, 1993). Therefore, high hopes were placed in the development of a PCR-based diagnosis. Following the sequencing of the genomes of several BSV species, highly species-specific primers targeting the RT-RNase domain of BSVs ORF3 were designed and used for PCR-based diagnosis (Harper *et al.*, 1996). Its outcome and additional evidence eventually lead to the finding that eBSVs were widespread in *Musa* genomes (Ndowora *et al.*, 1997; Harper *et al.*, 1999; Ndowora *et al.*, 1999) and that PCR was not suitable for diagnosing episomal forms of BSV in genotypes harboring the *M. balbisiana* genome due to the risk of false positives resulting from the amplification of eBSVs. In order to circumvent this problem, an immunocapture PCR (IC-PCR) diagnostic test was developed by Harper *et al.* (1999). It combines immunological capture of BSV particles by a polyclonal antiserum (Ndowora *et al.*, 1997) followed by a highly sensitive PCR step amplifying parts of the viral genome. The method has been optimized into a multiplex immunocapture PCR (M-IC-PCR; Le Provost *et al.*, 2006) combining the use of BSV-specific primers, that of primers specific of *Musa* genomic sequences whose role is to detect possible contaminations by *Musa* genomic DNA carrying eBSVs and that of DNase I to remove traces of genomic DNA and avoid false positives resulting from the amplification of eBSVs (Gambley, 2008; Chabannes *et al.*, 2013).

More recently, James *et al.* (2010; 2011) developed a diagnostic method based on rolling circle amplification (RCA), based on the use bacteriophage Phi29 DNA polymerase. This enzyme is specific of circular DNA molecules

and therefore, including episomal forms of viral genomes made of circular DNA (whether single or double stranded)

I-6. Objectives of the thesis

Control of black and yellow Sigatoka and pests of banana currently relies essentially on pesticides. Agro ecological alternatives are sought in order to limit the use of these pesticides, because such use is associated with hazards for the environment and for human health, and because it promotes the emergence of resistances among pest and pathogen populations and is therefore not sustainable. On the opposite, promising and sustainable agro ecological control strategies exist. They rely on the combination of genetically improved varieties with disease and pest resistance traits and agronomical practices such as fallows, use of service plants and removal of symptomatic leaves.

Breeding new varieties with pest and disease resistant traits is they key component of these strategies.

To this aim, several disease-resistant banana interspecific hybrid varieties were developed by various breeding programmes. These hybrid varieties have either triploid AAB or tetraploid AAAB genomes and harbor infectious eBSVs inherited from their *M. balbisiana* parent. The same applies to natural interspecific hybrids resulting from natural hybridization events. Although the risk of activating infectious eBSVs by cell culture is fairly well documented for both types (Dallot *et al.*, 2001; Côte *et al.*, 2010), nothing is known about the risk of spreading BSVs through the large scale field cultivation of such interspecific hybrids.

The purpose of this thesis is to contribute to the assessment of the risk of spreading banana streak viruses (BSVs) in the Dominican Republic through large scale cultivation of banana interspecific hybrids harbouring infectious endogenous BSV sequences. It focuses on the main interspecific hybrids grown in the Dominican Republic, the synthetic hybrid FHIA21 (AAAB) and the natural hybrid variety Macho x Hembra (AAB), two cooking type banana varieties that cover important acreages in the country.

To this aim, an unprecedented large scale prevalence study of the main BSV species was carried out on both FHIA-21 and Macho x Hembra throughout all producing areas of the Dominican Republic. A similar but more in depth study was carried out on the same varieties in two selected locations. This work was completed by a molecular analysis of the diversity of the mealybug species colonizing banana plants in the Dominican Republic. Chapter II presents the outcomes of this study and how its results shed new lights on the epidemiology of BSVs in the Dominican Republic.

A field experiment was set up on an unprecedented scale in order to study the kinetics of activation of infectious eBSVs in FHIA-21 and Macho x Hembra under field conditions and the correlation between activation and modes of production of banana planting material. In the course of this experiment, the impact of BSV infections on fruit production was also assessed. Chapter III presents the outcomes of this study, and their complementarity with those of the above mentioned prevalence study.

In concluding chapter IV, we discuss the impact of our results on the quantification of the risk of spreading BSVs through the cultivation of hybrid varieties carrying infectious eBSVs, and elaborate on strategies to mitigate this risk.



CHAPTER II

**PREVALENCE, DIVERSITY AND
TRANSMISSION OF BSVS IN THE
DOMINICAN REPUBLIC**

II-1. Context and objectives

Several banana varieties are cultivated in the Dominican Republic, amongst which two cooking types are grown almost exclusively for the domestic market: the natural AAB triploid plantain Macho x Hembra (MxH) and the synthetic AAAB tetraploid FHIA-21. Both are interspecific hybrids harboring the *M. balbisiana* genome. As such, they are suspected to host infectious eBSVs whose activation by biotic and abiotic stresses lead to spontaneous infections by cognate viruses (Dallot *et al.*, 2001; Côte *et al.*, 2010; Meyer *et al.*, 2008). Therefore, they have the potential to be the source of BSV outbreaks following possible large scale stress-related activation of infectious eBSVs triggered by environmental factors such as temperature differences or drought, e.g, under field cultivation conditions.

Although interspecific hybrids hosting infectious eBSVs have been grown for decades over thousands of hectares in several countries –especially in Cuba and the Dominican Republic- and the pathogenic potential of infectious eBSVs has been known since the pioneering work of Dallot *et al.* (2001), no study has ever been carried out to assess the risk of spreading BSVs through the cultivation of interspecific hybrids. The general objective of this thesis is to contribute to the assessment of this risk in the Dominican Republic for interspecific varieties Macho x Hembra and FHIA-21, which are both grown over thousands of hectares throughout the country.

The first step of this work was to gather data on the prevalence and transmission modes of the three most widespread BSV species (BSOLV, BSGFV and BSIMV) in FHIA-21 and MxH plantations throughout the Dominican Republic.

II-2. Prevalence of BSOLV, BSGFV and BSIMV in FHIA-21, Macho x Hembra and Cavendish in the Dominican Republic

II-2.1. Nationwide survey of the prevalence levels of BSOLV, BSGFV and BSIMV in FHIA-21 and MxH

A comprehensive and unprecedented nationwide survey was carried out in 57 plots scattered in 11 Dominican provinces, as shown in Fig. II-1. A total of 291 leaf samples from FHIA-21 and 299 leaf samples of MxH were collected from 28 and 29 distinct plots, respectively. Twenty of these collection sites were selected because they had adjacent FHIA-21 and MxH plots under strictly similar environmental conditions, enabling direct comparisons of BSVs prevalence levels between both varieties.

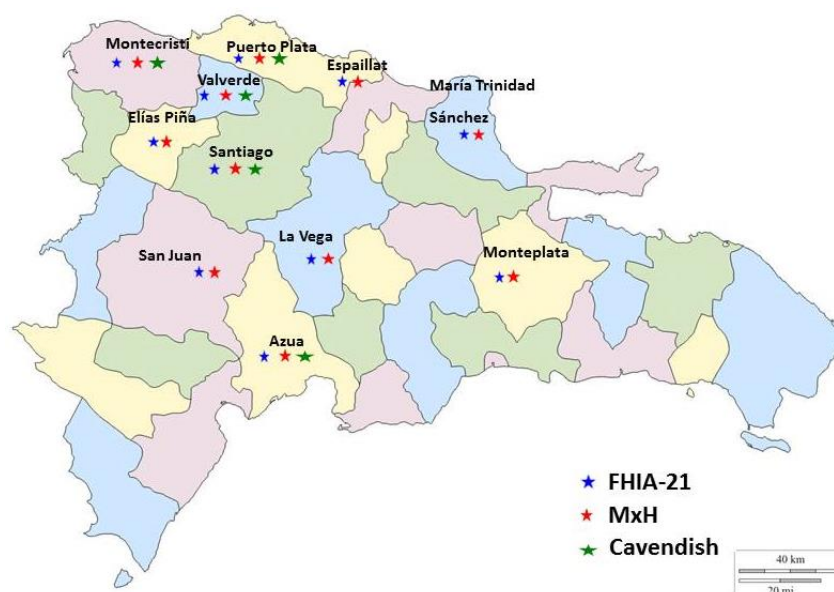


Figure II-1: Location of the sampling zones.

Red and blue arrows show collection sites for MxH and FHIA-21 leaf samples, respectively

All samples were indexed by multiplex immunocapture PCR (M-IC-PCR) for BSV species BSOLV, BSIMV and BSGFV. Each indexing experiment included infected samples used as positive controls (generously provided by Dr. M.-L. Iskra Caruana, CIRAD, France) as shown in Fig. II-2.

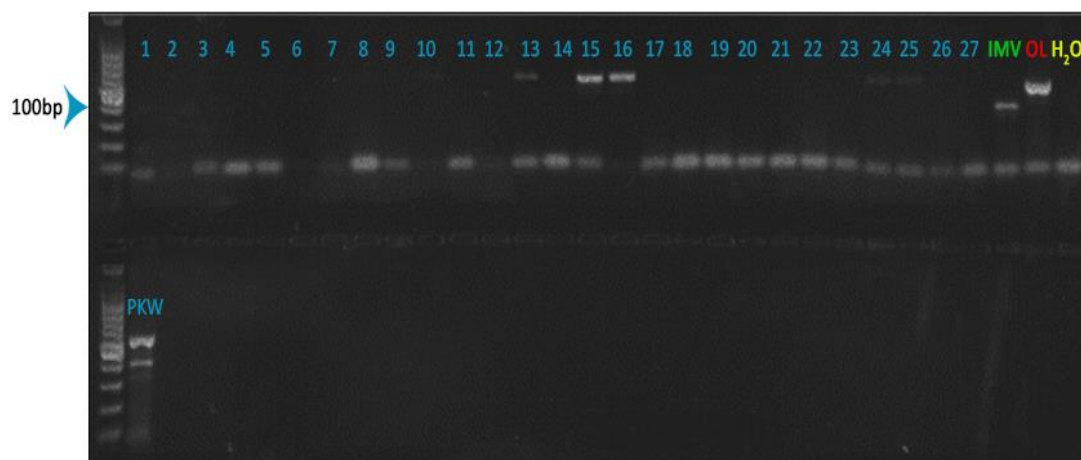


Figure. II-2: Detection of BSOLV by M-IC-PCR in FHIA-21 samples collected in the Dominican Republic.

Lanes 1-27: FHIA-21 samples; IMV: BSIMV-infected sample used to assess the specificity of the diagnostic; OL: BSOLV-infected positive control; H₂O: reaction mix only.

Every sample found infected was subjected to a second round of M-IC-PCR for confirmation. Tables II-1 and II-2 provide overviews of the results obtained for the collected FHIA-21 and MxH samples, respectively, and figure II-1 provides a graphical representation of these results. Full results are provided in Annexes 1 and 2.

As shown in tables II-2 and II-3, both BSGFV and BSOLV were detected in sampled plants, but BSIMV was not detected at all in any of the samples. BSGFV was the most prevalent species, infecting 19.59% of the total FHIA-21 samples and 4.01% of the total MxH samples, respectively, whereas species BSOLV was detected in 12.37% of the FHIA-21 samples and 0.67% of the MxH samples, respectively. These figures show that prevalence levels of BSGFV and BSOLV are significantly higher in FHIA-21 than in MxH in the sampled plots (see Fig. II-1). Co-infections by BSGFV and BSOLV were detected in 3% of the FHIA-21 samples but not in any of the MxH samples.

BSGFV was present in 23 of the 28 FHIA-21 sampled plots (82.1%) across all 11 sampled provinces and in 7 of the 29 MxH sampled plots (24.1%) across 5 of the 11 sampled provinces. BSOLV was present in 18 of the 28 FHIA-21 sampled plots (63.4%) across 10 of the 11 sampled provinces and in 2 of the 29 MxH sampled plots (6.9%) across 2 of the 11 sampled provinces. These figures also reflect that BSOLV and BSGFV are more prevalent in FHIA-21 than in MxH in the sampled plots, and show that these BSV species are well distributed throughout Dominican producing areas.

Taking into account only the 20 sampling sites where FHIA-21 and MxH plots are adjacent did not change the overall picture (Tables II-1 and II-2; Fig. II-3): BSGFV was detected in 20.19% of the FHIA-21 samples and in 3.35% of the MxH samples, whereas BSOLV was detected in 12.02% of the FHIA-21 samples and 0.42% of the MxH samples, respectively. BSGFV was present in 16 of these 20 FHIA-21 plots (80%) and in 5 of these 20 MxH plots (25%) whereas BSOLV was present in 6 of these 20 FHIA-21 plots (30%) and in 1 of these 20 MxH plots (5%).

A comprehensive range of criteria was registered for each sample and/or sampling site, including altitude, superficies of plot, nature of planting material (vitroplant, sucker), age of plot, plant density, irrigation system, association with other crops, weed control, presence of banana in nearby plots, extent of Black Sigatoka symptoms, presence of BSV symptoms on the plot, presence of mealybugs on the plot. However, attempts to establish statistically supported correlations between the presence / absence of BSOLV, BSGFV or BSIMV in samples and these various criteria proved unsuccessful. In particular, no significant correlation could be established between the presence of symptoms such as leaf streaks, pseudostem splitting, cigar or petiole necrosis (Fig. II-4) and the presence of BSVs, since the great majority of sampled plants later shown as infected by virus indexing were symptomless at the time of sampling. This observation sustains previous observations about the scarcity of symptoms in BSV-infected plants made during similar surveys carried out in Guadeloupe (Péréfarres *et al.*, 2009) and in Cuba (Javer Higginson *et al.*, 2014) and suggest that the impact of BSV infections is limited in both varieties in the Dominican Republic.

Table II-1: Overall results of the BSOLV, BSGFV and BSIMV nationwide prevalence survey in FHIA-21

Sampling site						FHIA-21								
Province	Municipality	Altitude (m)	Nature of planting material	Age of plot (years)	Presence of mealybugs on plot	Total collected samples	BSOLV		BSGFV		BSIMV		co-infected BSOLV + BSGFV	
							Positive samples	Proportion of collected samples (%)	Positive samples	Proportion of collected samples (%)	Positive samples	Proportion of collected samples (%)	Positive samples	Proportion of collected samples (%)
Azua	Azua	76	Suckers	4	No	11	0	0%	2	18,18%	0	0%	0	0%
Elias Piña	Comendador	398	Suckers	8	No	11	0	0%	1	9,09%	0	0%	0	0%
Españillat	Jababa	205	Suckers	5	Yes	10	1	10%	0	0%	0	0%	0	0%
	Rosa 2	157	Suckers	9	Yes	10	0	0%	0	0%	0	0%	0	0%
Hermanas Mirabal	Jayabo	258	Suckers	4	Yes	11	0	0%	0	0%	0	0%	0	0%
	Jayabo 2	248	Suckers	1	Yes	10	1	10%	2	20%	0	0%	0	0%
	Ceiba 1	133	Suckers	8	Yes	10	0	0%	3	30%	0	0%	0	0%
	Ceiba 2	149	Suckers	9	Yes	10	1	10%	1	10%	0	0%	0	0%
	Ceiba 3	148	Suckers	3	Yes	10	1	10%	1	10%	0	0%	0	0%
La Vega	Jamo	97	Suckers	1.5	Yes	10	3	30%	4	40%	0	0%	1	10%
	Barranca 1	108	Suckers	3	Yes	10	2	20%	0	0%	0	0%	0	0%
	Barranca 2	128	Suckers	3	Yes	9	0	0%	2	22%	0	0%	0	0%
	Barranca 3	84	Suckers	0.9	No	10	0	0%	0	0%	0	0%	0	0%
	Barranca 4	107	Suckers	1	Yes	11	0	0%	1	9,09%	0	0%	0	0%
Monte Plata	Bayaguana	86	Suckers	9	Yes	10	1	10%	5	50%	0	0%	1	10%
Montecristi	Jaramillo	20	Suckers	4	Yes	11	1	9%	5	45%	0	0%	1	9%
	Palo Verde	18	Vitroplants	10	Yes	10	3	30%	2	20%	0	0%	1	10%
Puerto Plata	La Balsa	24	Suckers	3	Yes	10	5	50%	2	20%	0	0%	0	0%
	Belloso	25	Suckers	1	Yes	10	3	30%	3	30%	0	0%	1	10%
San Juan	Pajonal	515	Suckers	6	Yes	10	1	10%	0	0%	0	0%	0	0%
Santiago	Banegas 1	144	Suckers	1.5	No	10	1	10%	1	10%	0	0%	0	0%
	Banegas 2	154	Suckers	3	No	11	1	9%	4	36,36%	0	0%	0	0%
	San Lorenzo 1	159	Suckers	1.6	Yes	10	2	20%	3	30%	0	0%	0	0%
	San Lorenzo 2	167	Suckers	1	Yes	11	1	9%	3	27%	0	0%	0	0%
Valverde Mao	Sabana grande	84	Suckers	1.5	Yes	11	2	18,18%	4	36,36%	0	0%	0	0%
	Boca de Mao	73	Suckers	2	Yes	12	3	25%	3	25%	0	0%	1	8%
	Esparanza	100	Suckers	3	Yes	11	0	0%	1	9,09%	0	0%	0	0%
	La Caida	27	Suckers	11	Yes	11	3	27,27%	4	36%	0	0%	1	9%
Total						291	36	12,37%	57	19,59%	0	0%	7	2%
20 plots adjacent to MxH						208	25	12,02%	42	20,19%	0	0%	5	2%

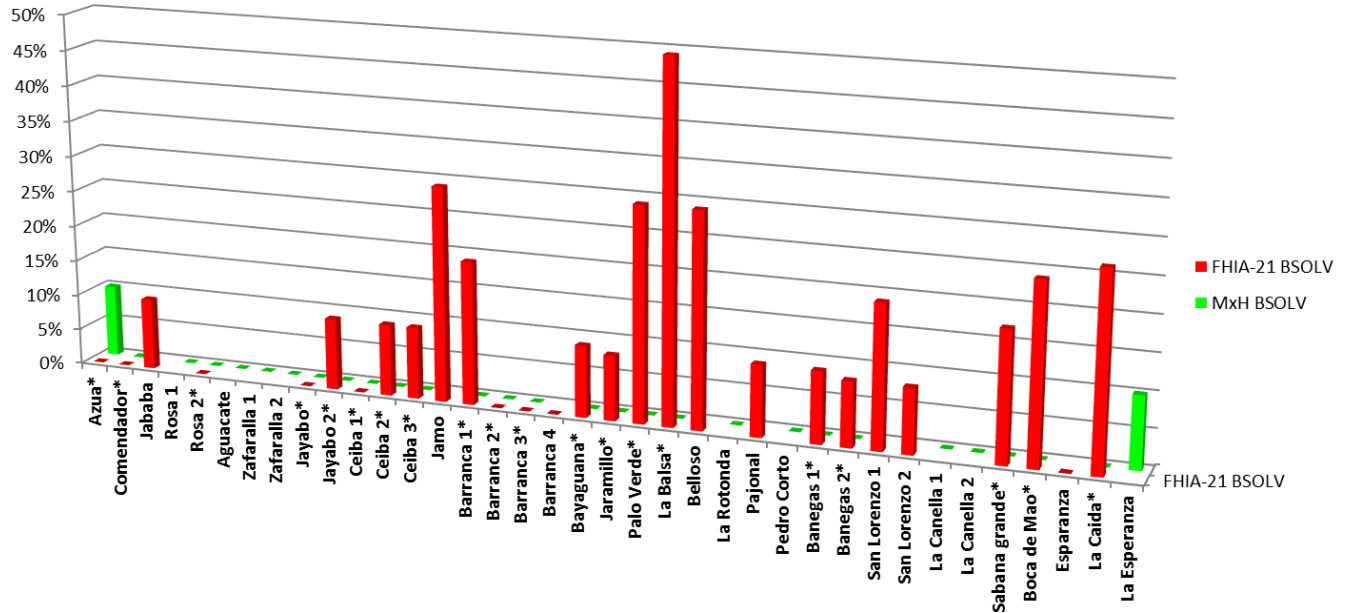
Sampling sites with adjacent FHIA-21 and MxH plots are highlighted in yellow

Table II-2: Overall results of the BSOLV, BSGFV and BSIMV nationwide prevalence survey in MxH

Sampling site						MxH								
Province	Municipality	Altitude (m)	Nature of planting material	Age of plot (years)	Presence of mealybugs on plot	Total collected samples	BSOLV		BSGFV		BSIMV		co-infected BSOLV + BSGFV	
							Positive samples	Proportion of collected samples (%)	Positive samples	Proportion of collected samples (%)	Positive samples	Proportion of collected samples (%)	Positive samples	Proportion of collected samples (%)
Azua	Azua	76	Suckers	4	Yes	10	1	10%	1	10%	0	0%	0	0%
Elias Pina	Commendador	395	Suckers	2	No	10	0	0%	1	10%	0	0%	0	0%
Espaillat	Aguacate	230	Suckers	1	No	10	0	0%	0	0%	0	0%	0	0%
	Rosa 1	177	Suckers	1	Yes	9	0	0%	0	0%	0	0%	0	0%
	Rosa 2	157	Suckers	4	Yes	11	0	0%	0	0%	0	0%	0	0%
	Zafaralla 1	180	Suckers	1	Yes	11	0	0%	0	0%	0	0%	0	0%
	Zafaralla 2	186	Suckers	1	No	11	0	0%	0	0%	0	0%	0	0%
Hermanas Mirabal	Jayabo	231	Suckers	10	Yes	10	0	0%	0	0%	0	0%	0	0%
	Jayabo 2	240	Suckers	12	No	10	0	0%	0	0%	0	0%	0	0%
	Ceiba 1	150	Suckers	5	Yes	10	0	0%	0	0%	0	0%	0	0%
	Ceiba 2	151	Suckers	6	Yes	10	0	0%	0	0%	0	0%	0	0%
	Ceiba 3	163	Suckers	1	Yes	11	0	0%	0	0%	0	0%	0	0%
La Vega	Barranca 1	101	Suckers	7	Yes	12	0	0%	0	0%	0	0%	0	0%
	Barranca 2	107	Suckers	9	Yes	11	0	0%	0	0%	0	0%	0	0%
	Barranca 3	107	Suckers	8.5	Yes	11	0	0%	0	0%	0	0%	0	0%
Monte Plata	Bayaguana	86	Suckers	2	Yes	10	0	0%	0	0%	0	0%	0	0%
Montecristi	Jaramillo	22	Vitroplants	3	Yes	8	0	0%	0	0%	0	0%	0	0%
	Palo Verde	18	Suckers	12	Yes	10	0	0%	0	0%	0	0%	0	0%
Puerto Plata	La Rotonda	19	Suckers	1	No	9	0	0%	3	33,33%	0	0%	0	0%
	La Balsa	24	Suckers	1	Yes	10	0	0%	3	30%	0	0%	0	0%
San Juan	Pedo Corto	415	Suckers	6	No	10	0	0%	0	0%	0	0%	0	0%
Santiago	Banegas 1	127	Suckers	1	No	10	0	0%	0	0%	0	0%	0	0%
	Banegas 2	150	Suckers	3	Yes	12	0	0%	1	8,33%	0	0%	0	0%
	La Canela 1	156	Suckers	0.9	Yes	10	0	0%	0	0%	0	0%	0	0%
	La canela 2	183	Suckers	3.5	Yes	10	0	0%	1	10%	0	0%	0	0%
Valverde Mao	Sabana grande	83	Suckers	1	No	9	0	0%	0	0%	0	0%	0	0%
	Boca de Mao	72	Suckers	2,5	No	13	0	0%	0	0%	0	0%	0	0%
	La Caida	73	Suckers	0,8	No	11	0	0%	2	18,18%	0	0%	0	0%
	La Esperanza	74	Suckers	1.3	Yes	10	1	10%	0	0%	0	0%	0	0%
Total						299	2	0,67%	12	4,01%	0	0%	0	0%
20 plots adjacent to MxH						239	1	0,42%	8	3,35%	0	0%	0	0%

Sampling sites with adjacent FHIA-21 and MxH plots are highlighted in yellow

A



B

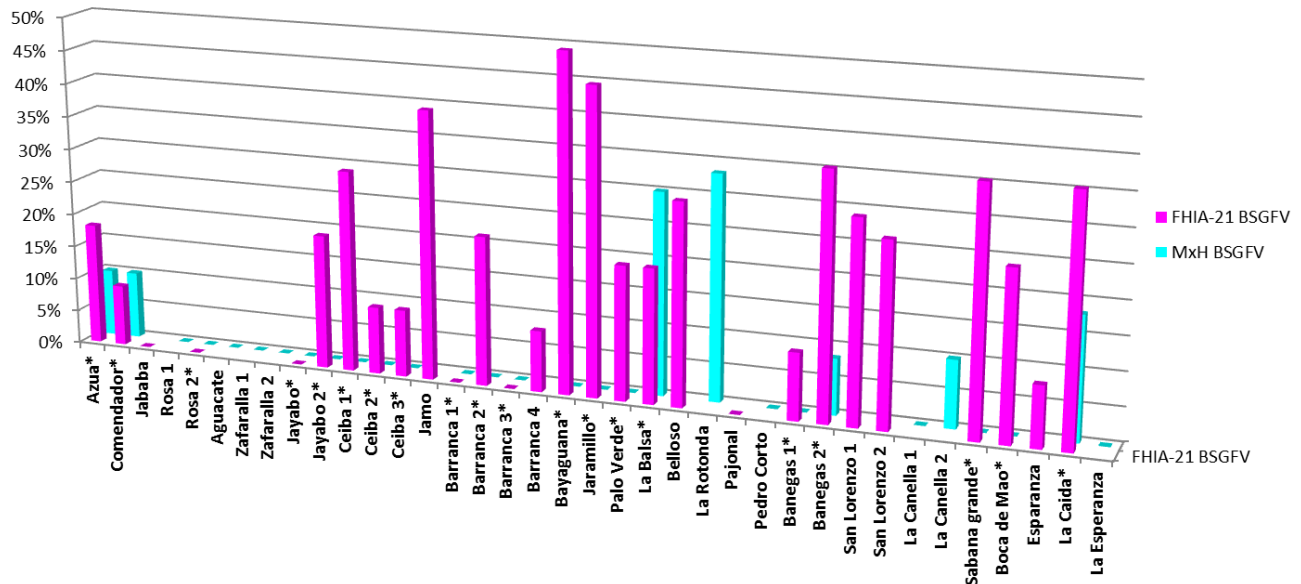


Figure II-3: Graphical representation of the results of the BSOLV and BSGFV nationwide prevalence survey in FHIA-21 and MxH

A: BSOLV survey

B: BSGFV survey

*: Sampling sites with adjacent FHIA-21 and MxH plots

Correlations between BSV infections and the nature of the planting material were also impossible to establish because the great majority of sampled plants (281/291 for FHIA-21 and 291/299 for MxH) originated from suckers. Considering that vegetative multiplication is one of the main propagation modes of viruses in plants and that farmers are not trained to control virus spread by eradication of symptomatic plants, higher prevalence rates of BSGFV and BSOLV were expected in sampled plants. This rather favorable situation results in the absence of epidemic hotspots among the sampled locations.

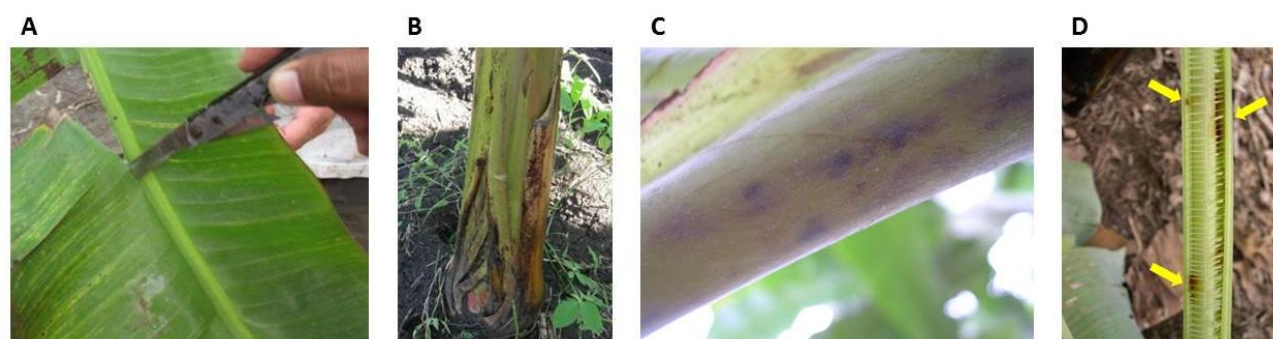


Figure II-4: BSV symptoms on leaf (A), pseudostem (B) and petiole (C, D) observed on FHIA-21 plants during the nationwide survey.

Yellow arrows point to internal necrosis symptoms observed in the section (D) of a petiole (C).

Source: R.T. Martinez, © IDIAF

II-2.2. In-depth survey of the prevalence levels of BSOLV, BSGFV and BSIMV in FHIA-21 and MxH in two selected locations

The two sampling locations showing the higher numbers of infected plants (Puerto Plata and Montecristi, see Fig. II-1) were selected for a more comprehensive survey of the prevalence levels of BSOLV, BSGFV and BSIMV in FHIA-21 and MxH.

This in-depth survey had three purposes:

- compare the influence of sampling scales on calculated prevalence levels : this comparison could be achieved for FHIA-21 in Puerto Plata (Belloso) and MxH in Montecristi (Palo Verde) since samples for both nationwide and in-depth surveys were collected on the same plots
- compare prevalence levels in FHIA-21 and MxH with those obtained during the nationwide prevalence survey
- compare the prevalence between plots where planting material originated from suckers or vitroplants: this could be achieved for the FHIA-21 plots in Montecristi (Jaramillo) and Puerto Plata (Belloso).

Table II-3: Overall results of the BSOLV, BSGFV and BSIMV in-depth survey in FHIA-21 and MxH

	Province	Municipality	Age or plot (year)	Total collected samples	Nature of planting material	Daily average temperature difference	BSOLV		BSGFV		BSIMV		co-infected BSOLV + BSGFV	
							Total positives	Proportion of collected samples	Total positives	Proportion of collected samples	Total positives	Proportion of collected samples	Total positives	Proportion of collected samples
FHIA-21	Montecristi	Jaramillo	10	100	Vitroplants	10.3°+/- 0.1°C	5	5%	29	29%	0	0%	1	1%
	Puerto Plata	Belloso	1	100	Suckers	9.3°C+/- 0.1°C	0	0%	31	31%	0	0%	0	0%
MxH	Montecristi	Palo Verde	12	100	Suckers	10.3+/- 0.2°C	0	0%	6	6%	0	0%	0	0%
	Puerto Plata	Belloso	2.5	100	Suckers	9.3°C+/- 0.1°C	1	1%	0	0%	0	0%	0	0%

Table II-4: Overall results of the BSOLV, BSGFV and BSIMV nationwide prevalence survey in Cavendish banana

Sampling site					Cavendish							
Province	Municipality	Nature of planting material	Age of plot (years)	Total collected samples	BSOLV		BSGFV		BSIMV		co-infected BSOLV + BSGFV	
					Positive samples	Proportion of collected samples (%)	Positive samples	Proportion of collected samples (%)	Positive samples	Proportion of collected samples (%)	Positive samples	Proportion of collected samples (%)
Azua	Finca 1	Sucker	15	18	0	0%	0	0%	0	0%	0	0%
	Finca 2	Sucker	15	20	1	5%	0	0%	0	0%	0	0%
	Finca 3	Sucker	10	20	1	5%	0	0%	0	0%	0	0%
	Finca 4	Sucker	15	20	2	10%	0	0%	0	0%	0	0%
Valverde Mao	Pueblo nuevo	Sucker	10	19	0	0%	0	0%	0	0%	0	0%
	Jaramillo	Sucker	15	15	0	0%	0	0%	0	0%	0	0%
	Montecristi	Sucker	10	39	0	0%	0	0%	0	0%	0	0%
	Palo Verde	Sucker	10	17	0	0%	0	0%	0	0%	0	0%
Puerto Plata	La Isabella	Sucker	4	20	0	0%	0	0%	0	0%	0	0%
Santiago	Banegas-1	Sucker	10	20	0	0%	0	0%	0	0%	0	0%
	Banegas-2	Sucker	6	20	0	0%	0	0%	0	0%	0	0%
	Banegas-3	Sucker	10	20	0	0%	0	0%	0	0%	0	0%
Total				248	4	1,61%	0	0%	0	0%	0	0%

Sample collection took place in October 2013, i.e 3 to 21 months following that of the nationwide survey, depending on sampling sites. In the meantime, FHIA-21 and MxH had been replaced in several of the sampled plots by other banana cultivars or other crops, or plots had been used as construction sites. This situation limited the choice of sampling sites for this in-depth survey and illustrates the rapid turnover of banana cultivation sites in the Dominican Republic. In the end, four sites were selected: for FHIA-21, samples were collected in Montecristi (Jaramillo) from plants originating from vitroplants and in Puerto Plata (Belloso) from plants originating from suckers; for MxH, samples were collected in Montecristi (Palo Verde) and in Puerto Plata (Belloso) and all of them originated from suckers. FHIA-21 collection site in Puerto Plata (Belloso) and MxH collection site in Montecristi (Palo Verde) were previously used for sampling during the nationwide survey.

Table II-3 provides an overview of the results of this survey. Full results are provided in Annexes 4 and 5. BSIMV was again not detected in any of the analyzed samples, confirming the results of the nationwide survey and suggesting that this viral species is probably not present in FHIA-21 and MxH in the Dominican Republic.

In Puerto Plata (Belloso), BSOLV and BSGFV were detected in 0% and 31% of the FHIA-21 samples, respectively. Respective figures of 30% and 30% were obtained on the same plot during the nationwide survey for BSOLV and BSGFV, respectively, but with sampling reduced to 10 plants which took place 17 months earlier. In Montecristi (Palo Verde), BSOLV and BSGFV were detected in 0% and 6% of the MxH samples, respectively. Respective figures of 0% and 0% were obtained on the same plot during the nationwide survey for BSOLV and BSGFV, but again with sampling reduced to 10 plants which took place 18 months earlier. Overall, these comparisons show that sampling size may influence calculations of BSOLV and BSGFV prevalence levels for the two considered collection sites, although samplings for both surveys were separated by a 17-18 months period that prevents strict comparisons. Discrepancies were also observed when comparing overall prevalence levels calculated from all collected samples in each survey: respective average BSOLV and BSGFV prevalence levels on FHIA-21 differed significantly, at 12.37% and 19.59% for the nationwide survey and 2.5% and 30% for the in-depth survey. On the other hand, respective average BSOLV and BSGFV prevalence levels on MxH were very similar: 0.67% and 4.01% for the nationwide survey, and 0% and 3.5% for the in-depth survey.

Prevalence levels calculated from the FHIA-21 samples originating from vitroplants (Montecristi, Jaramillo) and from suckers (Puerto Plata, Belloso) were also very similar. BSOLV prevalence levels were 5% and 0% for samples originating from vitroplants and suckers, respectively, whereas BSGFV prevalence levels were 29% and 31%, respectively. These figures show that BSGFV was significantly more prevalent than BSOLV in FHIA-21 in the analyzed samples, regardless of the mode of multiplication of the planting material. Interestingly, only two FHIA-21 plants infected by BSGFV were found infested by mealybugs. All other infected plants of the in-depth survey were mealybug-free, suggesting that BSV infections registered in the collected plants resulted either from the use of infected planting material or the activation of infectious eBSVs rather than from vector-mediated transmission. Attempts were made to sustain the latter hypothesis by correlating infections to temperature differences registered over a six months period preceding sample collection, since temperature differences are suspected to play a role in the activation of infectious eBSVs, but they were unsuccessful.

II-2.3. Survey of the prevalence levels of BSOLV, BSGFV and BSIMV in Cavendish dessert banana

Dessert banana of the Cavendish group have a triploid AAA genotype. Since the *M. acuminata* genome is devoid of infectious eBSVs, these banana types can only be infected by BSVs through infected planting material and/or vector-mediated virus transmission.

A survey of the prevalence levels of BSOLV, BSGFV and BSIMV was carried out in Cavendish dessert banana in order to gain insight into the dynamic of transmission of these viral species in the Dominican Republic. A total of 248 leaf samples were collected from 12 sampling sites scattered in 5 banana producing provinces, and then subjected to virus indexing. All sampled plants originated from suckers. Mealybugs were not controlled by insecticide treatment in any of these plots and farmers did not report any particular virus-related problem. Table II-4 provides an overview of the results of this survey. Full results are provided in Annex 5.

BSOLV was detected in only four of the analyzed samples whereas BSGFV and BSIMV were detected in none of them, leading to respective prevalence levels of 1.61%, 0% and 0%. These results suggest that BSOLV and BSGFV are present at very low levels in Cavendish dessert banana in the sampled areas because of a low transmission rate by mealybugs. BSOLV-infected samples were collected from three separate plots aged 10, 10 and 15 years, respectively. The absence of spread of BSOLV within these plots, even after such a long period of time, suggests a very low rate of vector-borne transmission either because mealybug species that have the potential to transmit BSVs are not present or because they are not moving or spreading much in these plots.

Furthermore, one of the many plots where no BSV-infected Cavendish banana was found (Banegas 1 - 10 years old) was adjacent to a couple of plots where BSOLV and/or BSGFV were detected during the nationwide survey: a 1.5 year old FHIA-21 plot harboring BSOLV and BSGFV prevalence rates of 10% each (1/10 plants) and a 1 year old MxH plot harboring a BSOLV prevalence rate of 4.5% (1/22 plant). This finding further suggests that vector-borne transmission of BSOLV and BSGFV (from interspecific hybrids to Cavendish in that instance) is low, although the FHIA-21 and MxH plots might not have been established for long enough to allow vector-borne transmission to take place. Importantly, none of the infected samples of this survey exhibited symptoms, confirming observations made on FHIA-21 and MxH during the nationwide and in-depth surveys that BSVs does not appear to have a noticeable impact on banana cultivation in the Dominican Republic.

II-3. eBSV patterns of FHIA-21 and MxH, and data on mealybug diversity provide hints into the epidemiology of BSVOL and BSGFV in the Dominican Republic

Data collected during the above mentioned surveys show that in the Dominican Republic BSOLV and BSGFV infections in FHIA-21 and MxH are sporadic and suggest that vector (mealybug)-borne transmission plays a limited role in their dynamics. This implies that infections arising in interspecific hybrid varieties FHIA-21 and MxH could rather result from the activation of infectious eBSVs. Interestingly, based on reported cases of BSV

outbreaks, Iskra Caruana *et al.* (2014a) hypothesized that sporadic resurgence of BSV species belonging to clade I (see Fig. I-13) for which infectious eBSVs exist could result from the activation of such infectious eBSVs following stresses, with no further spread of the disease.

In order to gain insight into the dynamic of BSOLV and BSGFV in the Dominican Republic, two key components of this dynamic were investigated: the structure of eBSVs in FHIA-21 and MxH, and the diversity of mealybug species in the FHIA21 plots sampled during the in-depth prevalence survey.

II-3.1. eBSV patterns of FHIA-21 and MxH

Leaf samples were randomly collected from 24 of the FHIA-21 plots and 25 of the MxH plots that were sampled during the nationwide survey. Total genomic DNA was extracted from all 49 samples and analyzed by PCR using the eBSV-specific markers developed by Gayral *et al.* (2008) and Chabannes *et al.* (2014). Multiple plants were purposely analyzed in order to assess that all samples from a given variety shared the same eBSV pattern, considering that mislabeling of varieties is frequent. Full results of the PCR analyses are provided in Annexes 6 to 8.

All analyzed samples did display identical eBSV patterns regardless of the variety. Their eBSOLV and eBSGFV patterns were the same as the one of diploid model species PKW (Gayral *et al.*, 2008; Chabannes *et al.*, 2013): they harbored infectious alleles OL1 and GF7 (Fig. II-5). Hence, BSOLV and BSGFV infections can occur in FHIA-21 and MxH either from mealybug-mediated transmission or from the activation of OL1 and/or GF7 infectious allele(s), whereas BSIMV infections can occur in both varieties solely through mealybug-mediated transmission.

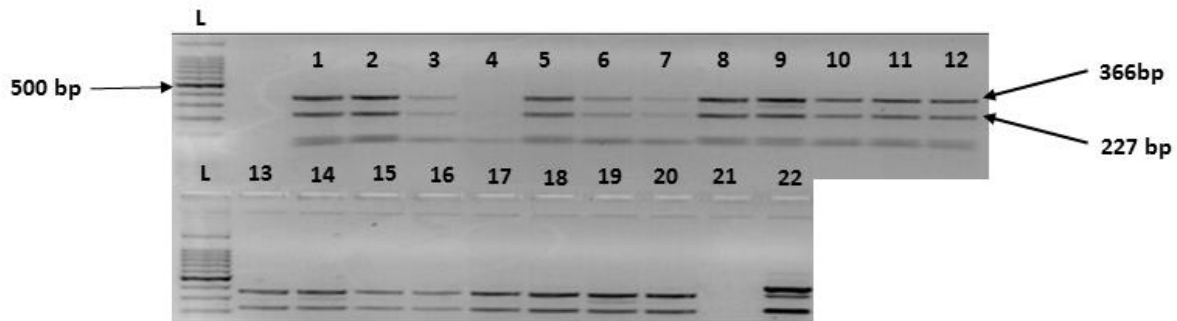


Figure II-5: eBSVs genotyping of FHIA-21 and MxH samples by PCR using dCAPS markers

Amplification products obtained using the DifGFF / DifGFR primer pair were digested by restriction enzyme HpyCH4III prior to electrophoresis. Size of digestion products is shown by arrows on the right side of figure; 500 bp band of DNA size marker is shown by an arrow on the left side of figure.

L: 100 bp DNA ladder; 1-10: FHIA-21 samples; 11-20: MxH samples; 21: reaction mix only; 22: Pisang Klutuk Wulung

II-3.2. Diversity of mealybug species

The diversity of mealybug species was assessed by PCR in the FHIA-21 and MxH plots that were sampled during the in-depth prevalence survey. Total genomic DNA was extracted from the 400 individual insects collected on these plots and used for PCRs using either generic primers or specific primers specific of species

Planococcus citri, *Planococcus ficus*, *Pseudococcus longispinus*, *Planococcus minor* or *Dysmicoccus brevipes*. All primers targeted the mitochondrial cytochrome c oxidase subunit I (COI).

A total of 297 samples gave rise to an amplification product of the expected size using generic primer pair TL2-N-3014 / CJ-J-2183. It is likely that the remaining 103 samples contained insufficient DNA quantities to raise PCR products. PCR products were also raised with primer pairs specific of *P. citri* (CitriFor1 / CitriRev1), *P. longispinus* (C1-J-2608 / TL2-N-3014) and *D. brevipes* (Dyb-1F / Dyb-1R).

Sequence comparisons included all mealybug COI sequences available from GenBank, except the one from *Saccharicoccus sacchari* because it overlaps only on a short stretch (137 bp) with the other 536 bp sequences used in our analyses. Figure II-7 shows the phylogenetic tree built from the alignment of selected amplified sequences representative of the two clades in which they all group. It shows that the representatives of the sequences amplified with primers specific of *P. citri* (MC30) and *P. longispinus* (P25) do not group with *P. citri* and *P. longispinus* COI sequences, respectively, casting doubts on the specificity of these primers. This situation may result from the fact that COI genes are highly conserved among mealybug species, displaying average homology levels above 86%, which make it difficult to design species-specific primers. Amplified sequences from the mealybugs collected on sampled FHIA-21 and MxH group in two clades on phylogenetic branches that are well supported by high bootstrap values. One of the clades does not group with any of the known mealybug species for which COI sequences are available; the other clade includes amplified sequences using either generic primers or *D. brevipes*-specific primers: these sequences share 99.4% and 99.1% homology with *D. neobrevipes* COI sequence, respectively, and 92.9% and 92.6% homology with *D. brevipes* COI sequence, respectively. It is likely that they arose from *D. neobrevipes*, which is very closely related to *D. brevipes*. Interestingly, none of these two clades groups with any of the mealybug species known to transmit BSVs, which do not seem to be represented in the mealybugs collected on FHIA-21 and MxH plants sampled during the in-depth survey. Comparing sequences of the large cluster to that of *S. sacchari* over the 137 bp sequence they share showed that they were 86% homologous, and that sequences from this cluster were not related to *S. sacchari*. Overall, our analyses further support the hypothesis that mealybug transmission might play a marginal role in the dynamics of BSVs in FHIA-21 and MxH in the Dominican Republic.

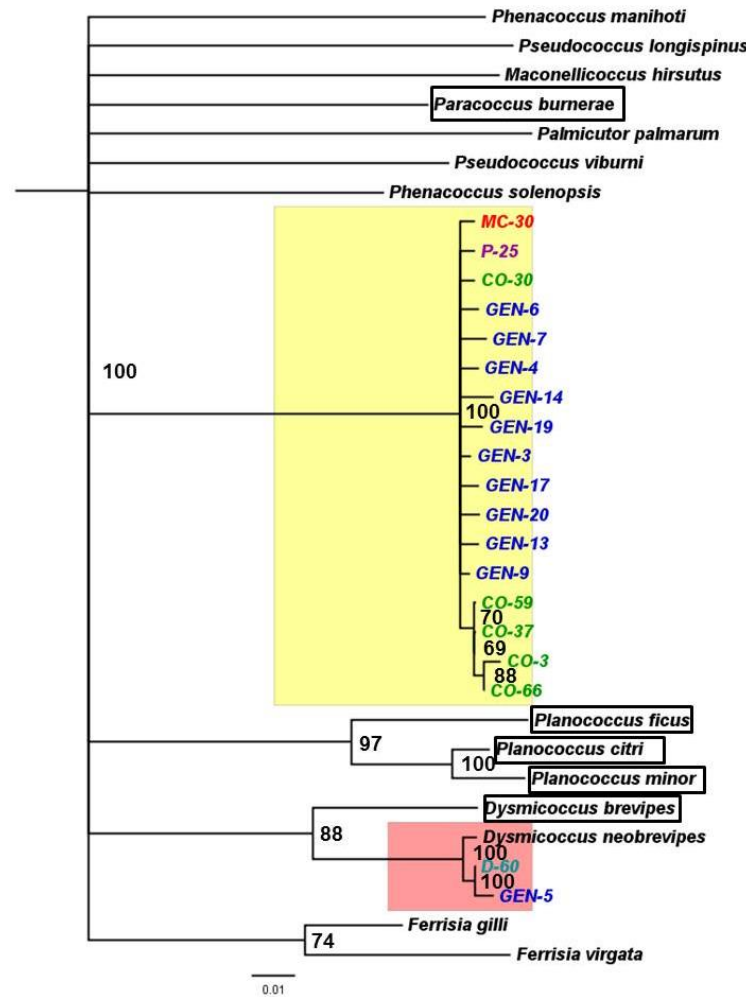


Fig II-6: Phylogenetic neighbor-joining tree built from partial 536 bp cytochrome C oxidase nucleotide sequences amplified from mealybug samples and from homologous sequences from known mealybug species.

Bootstrap values of 1,000 replicates are given above nodes when above 50 % (Tamura et al., 2004). Alignments were performed using CLUSTALW (Larkin et al., 2007) and phylogenetic tree was built with MEGA6 using the Neighbor-Joining method based on the HKY model (Hasegawa et al., 1985; Tamura et al., 2011). Only sequences displaying more than one substitution per base to each other were retained for the construction of the phylogenetic tree in order to avoid redundancy. The scale bar shows the number of substitutions per base. Partial cytochrome C oxidase sequences from mealybug species *Phenacoccus manihoti* (EU267196), *Palmicutor palmarum* (EU267218), *Pseudococcus longispinus* (EU267194), *Paracoccus burnerae* (FJ786962), *Maconellicoccus hirsutus* (EU267200), *Phenacoccus solenopsis* (EU267212), *Pseudococcus viburni* (EU267207), *Planococcus citri* (DQ238221), *Planococcus ficus* (DQ238220), *Dysmicoccus brevipes* (EU267214), *Dysmicoccus neobrevipes* (AF483206), *Ferrisia gilli* (EU267203) and *Ferrisia virgata* (EU267205) were used. Collected mealybugs are shown in the yellow and pink boxes

Selected sequences amplified from collected mealybugs are shown in the yellow and pink boxes. They were amplified using generic primer pairs C1-J-2183/TL2-N- 3014 (GEN and CO; Simon et al., 1994) and species-specific primer pairs CitriFor1 / CitriRev1 (MC; Rung et al., 2009) and Dybr/Dybf (D; Simon et al., 1994). COI sequences of mealybug species known to transmit BSVs are boxed.

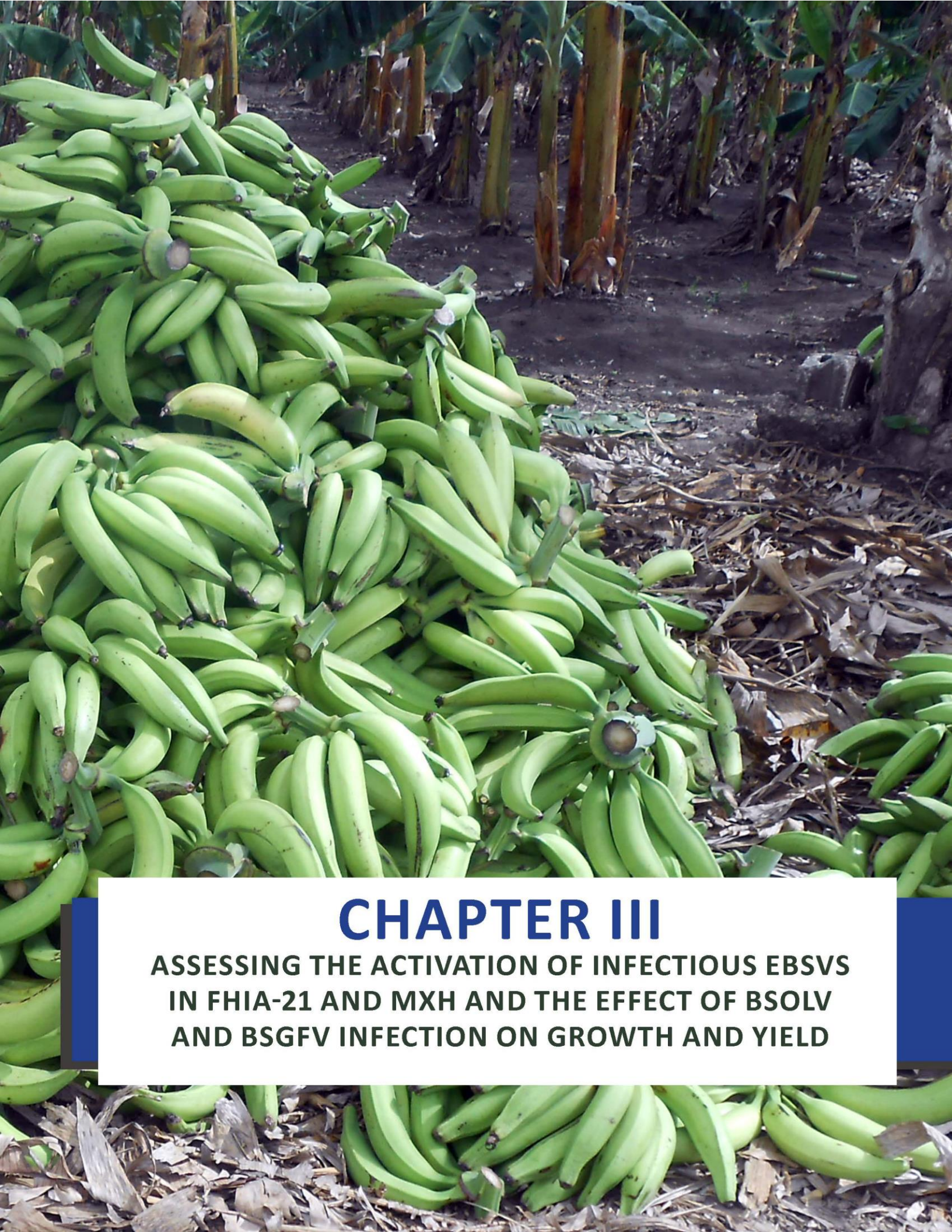
Key points of Chapter II

Prevalence of BSOLV, BSGFV and BSIMV in hybrids FHIA-21 and MxH and in Cavendish dessert banana in the Dominican Republic

- BSGFV is the most prevalent of the three targeted BSV species in all three surveyed varieties
- The highest prevalence levels were registered for BSGFV and BSOLV in FHIA-21
- Symptoms remain rare on infected plants
- BSIMV was not detected in any of the analyzed samples
- Very low prevalence levels registered on Cavendish banana suggest a very low transmission rate by mealybugs and/or by the distribution of infected planting material

Epidemiology of BSOLV and BSGFV in the Dominican Republic

- Both FHIA-21 and MxH carry infectious eBSOLV allele OL1 and eBSGFV allele GF7; both are devoid of the infectious eBSIMV sequence
- Mealybug species known to transmit BSVs are not present in the plants sampled during the in-depth survey, further supporting the hypothesis that vector-borne transmission might play a marginal role in the dynamics of BSVs in FHIA-21 and MxH in the Dominican Republic



CHAPTER III

**ASSESSING THE ACTIVATION OF INFECTIOUS EBSVS
IN FHIA-21 AND MXH AND THE EFFECT OF BSOLV
AND BSGFV INFECTION ON GROWTH AND YIELD**

III-1. Context and objectives

Data reported in the previous chapter suggest that BSV infections registered in FHIA-21 and in MxH in the Dominican Republic might result from the activation of infectious eBSVs. A similar hypothesis was formulated previously by Iskra Caruana *et al.* (2014a) on the basis of outbreak reports made on interspecific hybrid varieties in several locations worldwide.

In order to challenge this hypothesis, a field trial was established under cultivation conditions in Barranca (La Vega). The purpose of this experiment was:

- to quantify the activation rates of infectious alleles OL1 and GF7 in FHIA-21 and MxH over time under field cultivation conditions
- to compare the impact of the mode of production of planting material on activation rates
- to measure the impact of BSV infections on plant growth and fruit production

III-2. Production of the planting material

All plants were supplied by structures that do not control the sanitary status of mother plants by virus indexing, even when they produce large numbers of plants by cell culture.

Vitroplants were obtained from one single meristem originating from one single mother plant of either FHIA-21 or MxH. Suckers were obtained from several distinct mother plants; 6-8 suckers were collected from each mother plant.

Following a 2 months hardening phase in an insect proof greenhouse, various proportions of the plants were indexed for BanMMV, BBrMV, BBTv, BSGFV, BSIMV and BSOLV, depending on the expected outcome of the indexing process. For example, more plants were indexed for BSVs than for the other viruses because of the expected activation of eBSOLV and eBSGFV by cell culture (Dallot *et al.*, 2001; Côte *et al.*, 2010). Only plants indexed negative for BSVs were indexed for BanMMV, BBrMV and BBTv. Table III-1 provides an overview of the indexing results.

Table III-1: Virus indexing of the material produced for the experimental plot prior to planting

Virus	MxH*VP			MxH*S			FHIA-21*VP			FHIA-21*S			Williams*S		
	Total indexed plants	Infected plants	Proportion of indexed plants	Total indexed plants	Infected plants	Proportion of indexed plants	Total indexed plants	Infected plants	Proportion of indexed plants	Total indexed plants	Infected plants	Proportion of indexed plants	Total indexed plants	Infected plants	Proportion of indexed plants
BanMMV	90	0	0%	90	0	0%	90	0	0%	90	0	0%	232	0	0%
BBTV	90	0	0%	90	0	0%	90	0	0%	90	0	0%	232	0	0%
BBrMV	90	0	0%	90	0	0%	90	0	0%	90	0	0%	232	0	0%
BSGFV	105	0	0%	135	20	14,81%	105	0	0%	103	21	20,39%	232	0	0%
BSIMV	105	0	0%	105	0	0%	105	0	0%	105	0	0%	232	0	0%
BSOLV	135	2	1,48%	105	1	0,95%	105	4	3,81%	105	0	0%	232	0	0%
CMV	90	0	0%	90	0	0%	90	0	0%	90	0	0%	232	0	0%

All indexed plants were free of Banana *bunchy top virus* (BBTV) and *Banana bract mosaic virus* (BBrMV), which have not been reported in the Dominican Republic. They were also free of *Banana mild mosaic virus* (BanMMV) and *Cucumber mosaic virus* (CMV), which are known to occur in the country, and of BSIMV. On the opposite, FHIA-21 and MxH plants produced from either suckers or vitroplants were infected by BSOLV and BSGFV to various extents. MxH and FHIA-21 plants originating from vitroplants displayed respective BSOLV infection levels of 1.48% and 3.81% but were not infected by BSGFV. It is unlikely that these rather low infection levels result from vegetative transmission of BSOLV to daughter plants from the original and unique mother plants that were used for meristem culture, since vegetative transmission rates are usually higher. It is more likely that they result from the activation of eBSOLV infectious allele OL1 by cell culture, which has been reported in FHIA-21 (Dallot *et al.*, 2001) and in other natural AAB triploid plantains (Côte *et al.*, 2010). MxH and FHIA-21 plants produced from suckers displayed respective BSGFV infection rates of 14.81% and 20.31%. It is likely that a substantial proportion of suckers were collected from infected mother plants. On the opposite, only one MxH plant produced from suckers was infected by BSOLV.

III-3. Kinetics of activation of infectious alleles OL1 and GF7 in FHIA-21 and MxH under field conditions

In order to assess the kinetics of activation of infectious alleles OL1 and GF7 in FHIA-21 and MxH, an experimental plot was established in March 2014 using the above mentioned virus-free plants. The aim of this plot is to assess activation over two culture cycles (i.e over a 2 years period). Results presented in this thesis cover the first 15 months of the assay (March 2014 – June 2015).

In total, five types of planting materials were used and considered each a statistical treatment numbered T1 to T5:

- MxH vitroplants (MxH*VP): T1
- MxH suckers (MxH*S): T2
- FHIA-21 vitroplants (FHIA*VP): T3
- FHIA-21 suckers (FHIA*S): T4
- Williams vitroplants : T5

The experiment design was organized in 80 repeats randomized blocks, each containing one plant per type of planting material (T1 to T5) arranged in a random fashion (Fig. III-1). Each elementary plot (statistical unit) contained a single plant. The purpose of this experimental setup was to allow a 2x2 factorial analysis of the experiment (2 varieties * 2 modes of production of the planting material). Williams control plants (AAA genotype devoid of eBSVs) were used as internal controls in the blocks and also in an 84 plants external border to monitor mealybug-mediated transmission. They were subjected to BSOLV, BSGFV and BSIMV indexing as any other plant of the assay, but were not included in the statistical analysis since they were expected to

remain BSV-free. BSIMV infection rate was also used as a control to monitor mealybug-mediated transmission, since FHIA-21 and MxH do not host eBSIMV and can therefore become infected by BSIMV solely through insect-borne transmission; BSIMV infection rate was not included in the statistical analysis either, also because it was expected to remain nil.

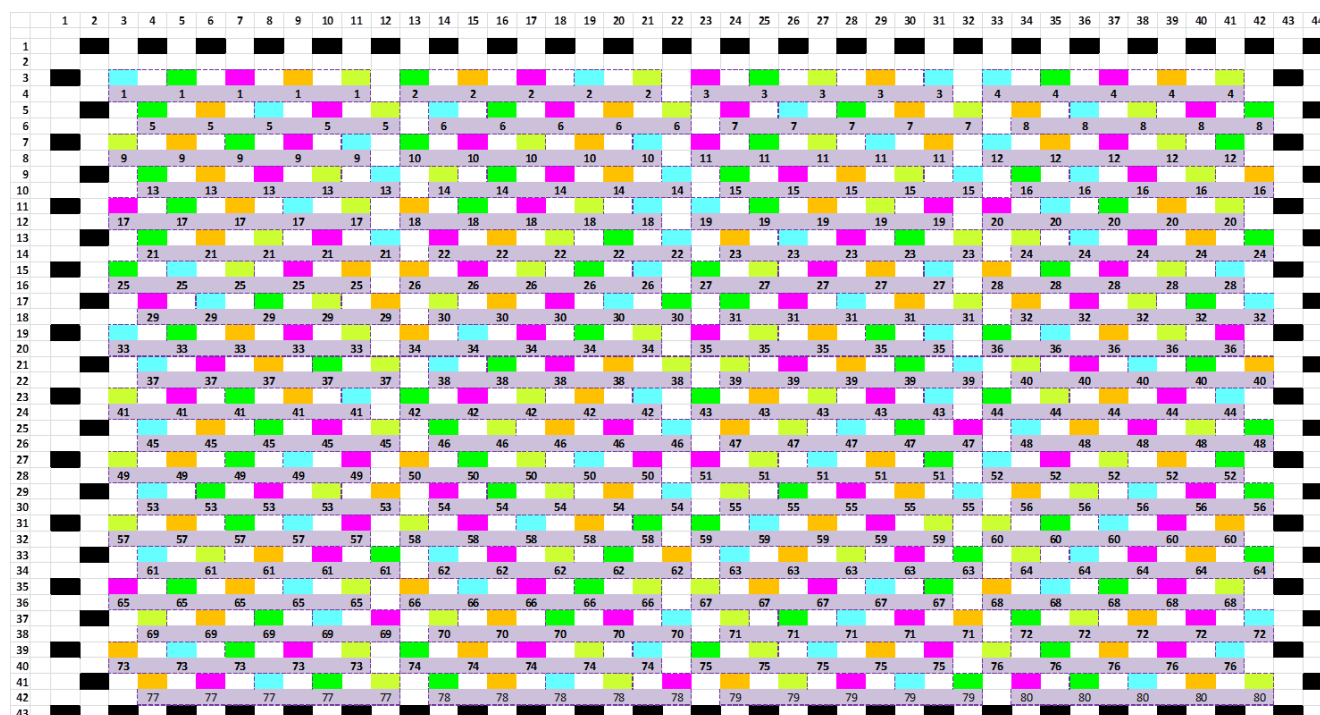


Figure III-1: organization of the experimental plot for the assessment of the activation rates of infectious eBSVs in FHIA21 and MxH hybrids under field conditions

Blocks are separated by dotted lines and numbered (1 o 80) in grey boxes. Random assignment of planting material for each experimental unit (one plant), within each block, is represented as colored boxes with the following color code:



III-3.1. Plant survival on plot

Death rates of plants at 15 months following their transfer to the experimental plot did not exceed 5% (4/80) per type of planting material (Table III-2) and the overall survival rate remained stable at 96% (384/400) from three months after planting onwards. Plant death did not significantly affect one type of planting material. Overall, these limited losses did not affect the ability to perform statistical analyses.

Table III-2: Survival of plants in the experimental plot at 15 months after planting

Planting material		Time											
Description	Code	Planting		3 months		6 months		9 months		12 months		15 months	
		Dead	Alive	Dead	Alive	Dead	Alive	Dead	Alive	Dead	Alive	Dead	Alive
MxH*VP	T1	0	80	4	76	4	76	4	76	4	76	4	76
MxH*S	T2	0	80	2	78	2	78	2	78	2	78	2	78
FHIA*VP	T3	0	80	4	76	4	76	4	76	4	76	4	76
FHIA*S	T4	0	80	3	77	3	77	3	77	3	77	3	77
Williams	T5	0	80	3	77	3	77	3	77	3	77	3	77
Total		0	400	16	384	16	384	16	384	16	384	16	384

III-3.2. Temporal patterns of infections

The number of plants infected by BSOLV, BSGF and BSIMV was monitored by viral indexing every three months.

None of the Williams plants (80 plants from the experimental plot, reduced to 77 plants from month 3, and 84 plants from the external border) was infected by any of the three studied BSV species. This negative result suggests a total absence of mealybug-mediated transmission on the plot, probably resulting from the chemical control of mealybugs and ants. Likewise, none of the plants of the assay was infected by BSIMV, as expected. Therefore, it is assumed that infections arising on MxH and FHIA-21 result from the activation of infectious alleles OL1 and GF7.

Table III-3 shows the evolution of the number of BSOLV- and BSGFV-infected MxH and FHIA-21 plants over the considered 15 months period. Full indexing results are provided in Annex 9.

Table III-3: Evolution of the number of BSOLV- and BSGFV infected FHIA-21 and MxH plants of the experimental plot over a 15 months period.

		BSOLV (A)						BSGFV (B)						BSOLV or BSGFV (C)					
		0 month	3 months	6 months	9 months	12 months	15 months	0 month	3 months	6 months	9 months	12 months	15 months	0 month	3 months	6 months	9 months	12 months	15 months
MxH*Vp	T1	0	0	0	0	0	2	0	0	1	2	4	7	0	0	1	2	4	9
MxH*S	T2	0	0	0	0	2	2	0	0	2	3	3	6	0	0	2	3	4	7
FHIA*Vp	T3	0	0	2	2	2	2	0	0	3	5	9	15	0	0	5	6	10	16
FHIA*S	T4	0	0	0	0	2	3	0	0	4	5	5	7	0	0	4	5	7	9
Williams	T5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total		0	0	2	2	6	9	0	0	10	15	21	35	0	0	12	16	25	41

Figure III-1 provides a graphical representation of the evolution of infection rates over time, measured through the percentage of MxH and FHIA-21 plants infected by BSOLV and BSGFV.

No infected plant was detected for the first 3 months following the transfer of plants to the plot. The first infected samples were detected at 6 months after planting, which means that infections occurred between 3 and 6 months after planting. From then on, the total number of infected plants increased steadily from 12 at month 6 to 16 at month 9, 25 at month 12 and 41 at month 15.

A total of 15 plants were infected by BSGFV at harvest time (2 MxH*vitroplants, 3 MxH*sucker, 5 FHIA-21*vitroplant and 5 FHIA-21*sucker). Their respective daughter plants, used as ratoon crops for the following cycle, were also infected at the following time point. Similar observations were made for the 2 plants originating from MxH suckers that were infected by BSOLV at harvest time. These observations confirm those made by Daniells *et al.* (2001) that the rate of BSV transmission through suckers is 100%.

Maximum BSOLV infection rate was 3.94% (4/76) for FHIA-21 suckers. Two infected plants were also registered for MxH vitroplants (2.63%), FHIA-21 vitroplants (2.63%) and MxH suckers (2.56%). Overall, these figures suggest that the activation rate of infectious allele OL1 in MxH and FHIA-21 is low under the conditions of the assay. The curves (Fig. III-1A) seem to have reached a plateau (FHIA-21 vitroplants, MxH suckers) or to be reaching it (FHIA-21 suckers) although additional time points are needed to draw a definite conclusion in this regard.

Considering the reduced number of plants infected by BSOLV, statistical analyses could not be performed on the BSOLV variable.

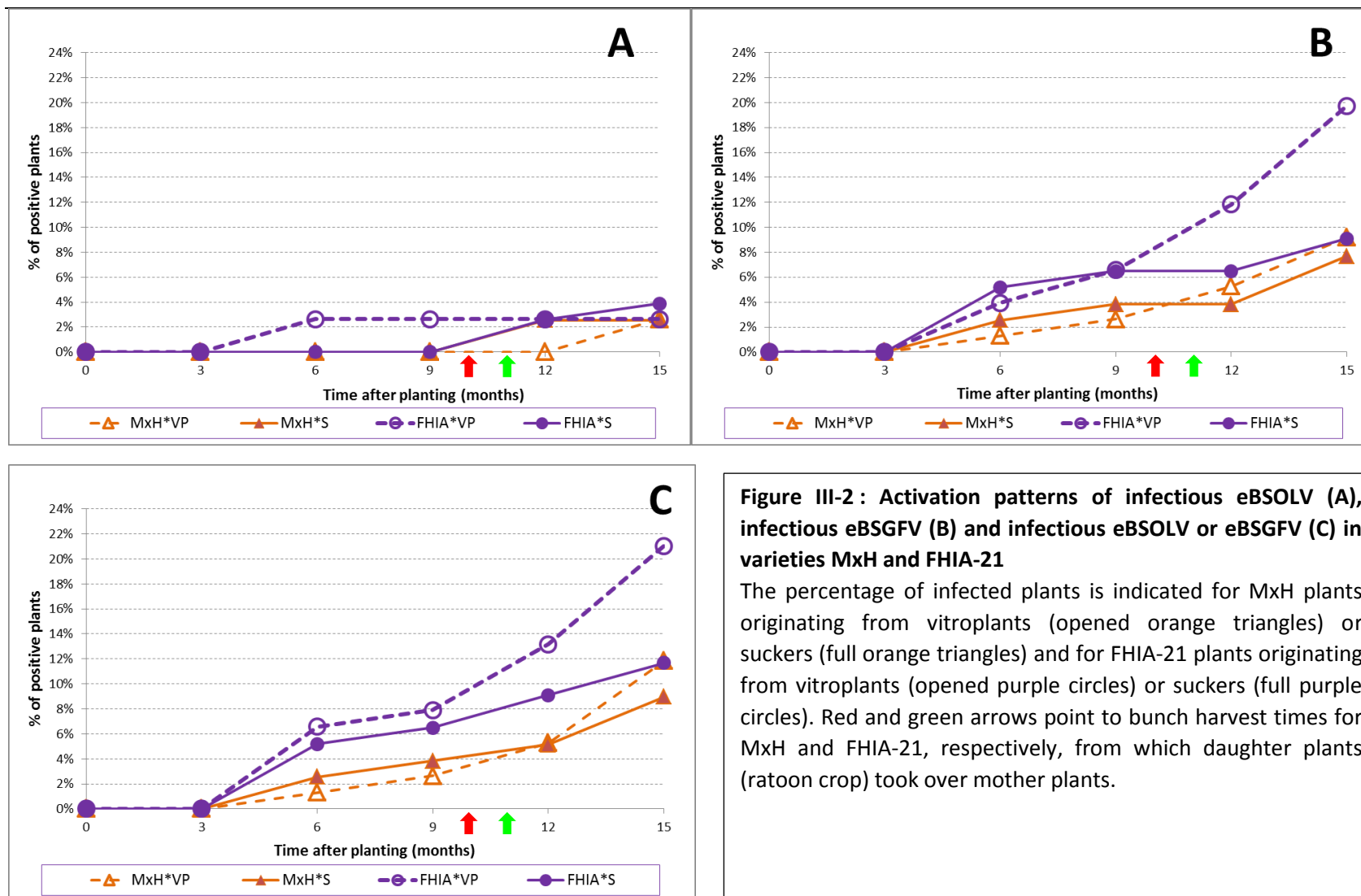


Figure III-2 : Activation patterns of infectious eBSOLV (A), infectious eBSGFV (B) and infectious eBSOLV or eBSGFV (C) in varieties MxH and FHIA-21

The percentage of infected plants is indicated for MxH plants originating from vitroplants (opened orange triangles) or suckers (full orange triangles) and for FHIA-21 plants originating from vitroplants (opened purple circles) or suckers (full purple circles). Red and green arrows point to bunch harvest times for MxH and FHIA-21, respectively, from which daughter plants (ratoon crop) took over mother plants.

Patterns of infection by BSGFV told a very different story (Fig. III-1B). Overall, registered BSGFV infection rates were higher than for BSOLV for the four types of planting material. Maximal infection rate was registered for FHIA-21 vitroplants, reaching 19.7% at 15 months. Lower but significant rates were registered for MxH vitroplants (9.2%), FHIA-21 suckers (9.1%) and MxH suckers (7.7%). Overall, infection rates progressed faster for vitroplants, although additional time points will tell if this trend will be sustained over time. Combining BSOLV and BSGFV infection rates (Fig. III-1C) provided a similar pattern as the one observed for BSGV infections alone, confirming that infection rates are higher in FHIA-21 vitroplants than in any other plant material used in the assay.

Logistic regression of the BSGFV infection rate at 15 months with two crossed factors (variety and mode of multiplication of the planting material) did not reveal significant main effects. However, tests sliced by factor levels showed that the influence of the mode of multiplication on infection rates is slightly significant for FHIA-21 ($P = 0.068$) but not for MxH ($P = 0.739$). Likewise, analyses showed that the higher BSGFV infection rate registered for FHIA-21 vitroplants compared to that of MxH vitroplants was also statistically slightly significant ($P = 0.072$). More parameters and results of these analyses are detailed in Annex 10.

Overall, these results, although still preliminary, are biologically meaningful and suggest that activation rates of infectious allele GF7, measured through BSGFV infection rates, are higher than that of infectious allele OL1 measured through BSOLV infection rates, regardless of both the variety and the mode of multiplication of the planting material. This situation presents similarities with that described by Côte *et al.* (2010) who reported on differential activation rates of infectious eBSOLVs and eBSGFVs by cell culture for the tetraploid interspecific hybrid (AAAB) CRBP39. Interestingly, differential activation also occurred for CRBP39 during culture under field conditions, but the situation was the exact opposite, with infectious eBSGFV being activated by culture conditions while infectious eBSOLV was not (Côte *et al.*, unpublished). Our results suggest that field culture conditions are also a strong activator of infectious allele GF7 but that they are a weak activator of infectious allele OL1. They also suggest that activation levels of infectious allele GF7 differ between interspecific varieties with identical eBSGFV patterns but with different genetic backgrounds, sustaining the hypothesis formulated by Lheureux *et al.* (2003) that additional factors to infectious eBSVs play a role in the activation process.

III-3.3. Symptoms of BSV infection

All the plants of the assay were inspected visually for BSV symptoms every three weeks until flowering, then every month. No symptoms were observed on the Williams control plants (77 plants in the randomized blocks and 84 plants in the external border). The earliest typical BSV symptoms of chlorotic leaf streaks and pseudostem splitting (illustrated on Fig. II-1A and II-1B) were observed on FHIA-21 plants before flowering. The number of symptomatic FHIA-21 and MxH plants increased over time to a maximum of 5.2% (16/307) at 15 months after planting (see Table III-4). However, indexing results showed once again that the correlation between symptoms and infection is poor: only 5 of the 16 symptomatic plants were indexed positive, including the 3 only plants of the assay that were co-infected by BSOLV and BSGFV, although a total of 41 plants were indexed positive at that time.

Table III-4: Correlation between symptoms and virus indexing results at 15 months after planting

	Planting material				Symptoms appeared at timepoint (months after planting)						Symptoms		Indexing results		
Plant number	MxH*VP (T1)	MxH*S (T2)	FHIA-21*VP (T3)	FHIA-21*S (T4)							Leaf streaks	Pseudostem splitting	BSOLV	BSGFV	BSIMV
					0	3	6	9	12	15					
23													+	+	-
37													-	-	-
68													-	-	-
56													-	-	-
78													-	-	-
96													-	-	-
306													-	-	-
177													-	-	-
210													-	-	-
215													-	-	-
128													+	+	-
337													-	-	-
375													+	-	-
105													-	+	-
373													-	-	-
304													+	+	-

Average temperature over the 15 months period of the assay, was 28°C and may have contributed to lower the expression of BSV symptoms. Dahal *et al.* (1998) reported that 28-35°C temperatures were optimal for the expression of BSV symptoms on other interspecific hybrid varieties, and decreased symptom severity was observed at temperatures lower than 28°C.

III-4. Effect of BSOLV and BSGFV infection on the growth and yield of MxH and FHIA-21 in the Dominican Republic

Attempts were made to evaluate the impact of BSOLV and BSGFV infection on several agronomical parameters of MxH and FHIA-21 plants (height and girth of the pseudostem) and fruit bunches (number of hands, number of fingers, fruit girth, bunch weight). However, only 2 plants were infected by BSOLV and 15 by BSGFV at harvest time at the end of the first cycle (see Table III-5; see Annex 11 for full results). Considering these low frequencies, only BSGFV-infected plants could be used for statistical analyses. Moreover, possible bias in the data for the number of hands and number of fingers led to their exclusion from further analyses. Still, mean values and standard errors for the remaining parameters (plant height, pseudostem girth and bunch weight) should be handled with care since they were calculated from very different numbers of plants (more than 70 for non-infected plants vs 2-5 for infected plants).

Table III-5: Descriptive statistics for three agronomical variables within each treatment

			Plant height (cm)		Pseudostem girth (cm)		Bunch weight (Kg)	
Treatment	BSGFV	Number	Mean	Std Dev	Mean	Std Dev	Mean	Std Dev
MxH*VP (T1)	Non-infected	74	291.4	21.7	55.41	5.18	13.53	2.20
	Infected	2	306.0	4.2	55.50	10.61	15.00	0.00
MxH*S (T2)	Non-infected	75	292.8	22.0	55.01	6.17	13.96	2.65
	Infected	3	289.3	23.0	58.00	1.73	15.00	4.58
FHIA*VP (T3)	Non-infected	71	293.2	24.9	55.61	5.76	13.80	2.71
	Infected	5	289.0	22.9	51.00	10.37	12.60	1.52
FHIA*S (T4)	Non-infected	72	293.1	25.0	55.46	5.48	13.89	2.20
	Infected	5	295.2	19.1	51.60	2.61	13.00	2.35

Std dev : standard deviation

Descriptive statistics did not reveal clear trends in differences between plant height of infected and non-infected plants (Table III-5). A decrease (above the 5% threshold) in pseudostem girth and bunch weight was observed in infected FHIA-21, although once again the low number of infected plants (5 FHIA*VP and 5 FHIA*S) precludes any definite conclusions. Moreover, dotplots of individual values distribution for these parameters did not show any particular distribution pattern of infected plants compared to non-infected plants (Fig. III-2).

Therefore, based on preliminary statistical data, no significant detrimental effects of BSOLV and BSOLV infection on the growth and production of MxH and FHIA could be reported, although these observations need to be confirmed on larger batches of infected plants.

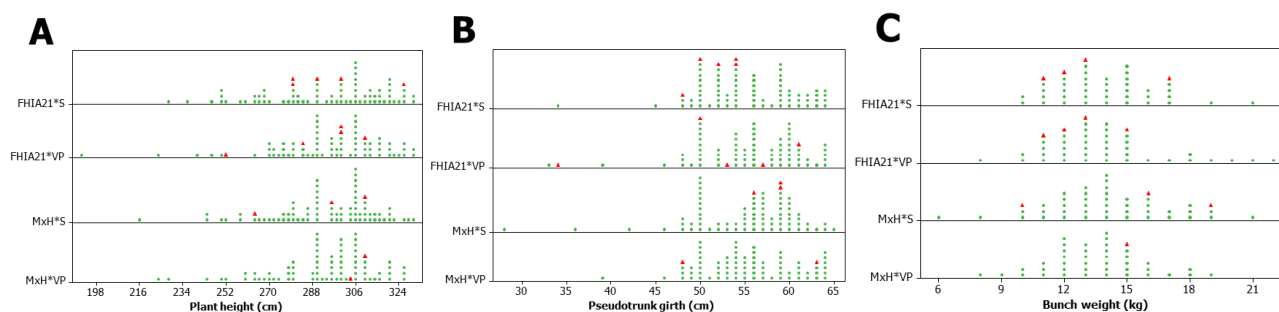


Figure III-3: Point diagrams showing the distribution of individual agronomical parameters for the FHIA-21 and MxH plants of the experimental plot.

▲: infected plant; ●: non-infected plant

Key points of Chapter III

Kinetics of activation of infectious alleles OL1 and GF7 in FHIA-21 and MxH under field conditions

- Increasing infection rates were registered over time for FHIA-21 and, to a much lesser extent, for MxH but no infection was registered for the Williams control plants, suggesting that registered infections arose from the activation of infectious alleles OL1 and GF7
- Under the experimental conditions of the plot, field culture conditions are a strong activator of infectious allele GF7 but a weak activator of infectious allele OL1 in MxH and FHIA-21
- Differential activation levels in MxH and in FHIA-21 for infectious alleles OL1 and GF7 suggest that genetic background plays a role in the level of activation of these alleles
- The rate of transmission of BSOLV and BSGFV from mother plants (plant crop) to daughter plants (ratoon crop) was 100%

Effect of BSOLV and BSGFV infection on the growth and yield of MxH and FHIA-21 in the Dominican Republic

- The presence of symptoms was poorly correlated with actual infection by either BSOLV or BSGFV in MxH and FHIA-21
- No significant detrimental effect of BSGFV infection on plant growth and fruit production was measured, although the low number of infected plants at bunch harvest time precludes definite conclusions.



CHAPTER IV

CONCLUSION & PERSPECTIVES

Since the discovery endogenous viral elements (EVEs) in plants almost 20 years ago (Bejarano *et al.*, 1996), hundreds of plant EVEs have been characterized. However, only a handful of them are infectious (Teycheney & Geering, 2011). The most economically important ones are infectious endogenous *Banana streak virus* (eBSV) sequences that are present in the genome of *Musa balbisiana* (Iskra-Caruana *et al.*, 2006), one of the main progenitors of interspecific hybrid varieties. Their activation by biotic and abiotic stresses lead to spontaneous infections by their cognate virus in natural and created triploid (AAB) and tetraploid (AAAB) banana interspecific hybrids and are supposed to play a key role in sporadic BSV outbreaks (Iskra-Caruana *et al.*, 2014a). Since their discovery in the late 1990's (Ndowora *et al.*, 1999; Harper *et al.*, 1999) infectious eBSVs have become the main constraint for breeding new banana varieties and a major concern for deploying interspecific banana hybrids, due to the risk of outbreak that could result from their large scale activation under field conditions.

Because of to their overall qualities, especially their high level resistance to Black Sigatoka -the most devastating leaf fungal disease of banana- interspecific hybrids created by the Honduran Foundation for Agricultural Research (FHIA) have been widely distributed and grown for decades over large areas in the Caribbean (Cuba, the Dominican Republic), Latin America and Africa. However, the risk of spreading BSVs through large scale cultivation of these hybrids has never been assessed; it has never been assessed either for natural interspecific hybrids which are equally prone to activation of infectious eBSVs (Côte *et al.*, 2010) and are cultivated on even larger areas worldwide. This issue was tackle in this thesis, whose purpose was to contribute to the assessment of the risk of spreading BSVs through large scale distribution of the two main banana cooking type interspecific hybrids cultivated in the Dominican Republic, the tetraploid (AAAB) hybrid FHIA-21 and the triploid (AAB) hybrid Macho x Hembra (MxH).

IV-1. Differential prevalence levels and insights into the epidemiology of BSVs in the Dominican Republic

An extensive nationwide survey was carried out in the Dominican Republic in order to monitor for the first time the levels of prevalence of the three most widespread BSV species -*Banana streak OL virus* (BSOLV), *Banana streak GF virus* (BSGFV) and *Banana streak IM virus* (BSIMV)- in MxH and FHIA-21 throughout all the banana producing areas of the country. A limited number of samples were collected from a large number of sites, in order to provide a snapshot of the epidemiological situation of the Dominican Republic vis à vis BSVs. This survey led to the first detection of BSVs in the Dominican Republic. It showed that BSGFV is the most prevalent of the three targeted BSV species in both FHIA-21 and MxH and that prevalence levels of BSGFV and BSOLV are substantially higher in FHIA-21 than in MxH. It also provided evidence that BSIMV, whose transmission in interspecific hybrids is thought to result primarily from the activation of infectious eBSIMVs (Lheureux *et al.*, 2003; Geering *et al.*, 2011; Chabannes *et al.*, 2013), is not present in the Dominican Republic. A thorough molecular analysis of the eBSV pattern of sampled FHIA-21 and MxH plants showed that both

varieties are devoid of eBSIMV, and that both harbor infectious alleles OL1 (eBSOLV) and GF7 (eBSGFV). A medium scale BSOLV, BSGFV and BSIMV prevalence survey was carried out on Cavendish dessert banana, which is devoid of infectious eBSVs and can therefore become infected only through mealybug-mediated transmission or the use of infected planting material. Very low prevalence levels were registered for both BSOLV and BSGFV, and BSIMV was not detected at all, pointing again to a marginal role of mealybugs or the use of contaminated planting material in the epidemiology of BSVs in the Dominican Republic. A molecular taxonomical survey carried out on mealybugs sampled during one of the surveys suggested, that mealybug species known to transmit BSVs were not present on the sampled plants, further supporting the hypothesis that vector-borne transmission plays a marginal role in the dynamics of BSOLV and BSGFV in FHIA-21 and MxH, in the Dominican Republic and that BSOLV and BSGFV infections more likely result from the activation of infectious eBSVs. In this regards, it can be hypothesized that the differences observed in MxH and FHIA-21 between the prevalence levels of BSGFV and to a lesser extent that of BSOLV could result from differential activation levels of infectious alleles OL1 and GF7 triggered by abiotic stresses under field conditions, since both MxH and FHIA-21 share identical eBSOLV and eBSGFV patterns. Differential activation of infectious eBSVs was also proposed by Côte *et al.* (2010) for another tetraploid (AAAB) hybrid, CRBP 39, during cell culture. Such a differential activation could involve additional factors such as the BSV expression locus (BEL) hypothesized by Lheureux *et al.* (2003).

IV-2. Evaluation of the risk of spreading BSOLV and BSGFV through the cultivation of MxH and FHIA-21 in the Dominican Republic

Considering that risk can be defined as the product of the probability and consequence of a hazardous event or phenomenon, the risk of spreading BSOLV and BSGFV through large scale distribution of FHIA-21 and MxH can be defined as the product of the probability of activation of infectious alleles OL1 and GF7 and the consequence of such an activation. As such, this risk can be quantified by measuring the proportion of BSOLV and BSGFV infections resulting from the activation of infectious alleles OL1 and GF7 and the impact of these infections on banana production. An experimental plot was set up in order to monitor both factors in MxH and FHIA-21 and contribute to the evaluation of this risk for both varieties. It is the first assay of its kind ever carried out worldwide.

This assay will be monitored over at least 2 production cycles, of which results reported in this thesis cover the first 15 months. During this period, significantly different activation levels were monitored for infectious allele GF7 in FHIA-21 and MxH, sustaining the hypothesis that field culture triggers differential activation of eBSV infectious alleles. Both the mode of multiplication of the planting material and the variety influenced activation levels. The highest activation rate was monitored in FHIA-21 plants originating from vitroplants at 15 months after planting: 19.7% of the plants were infected, which compares to 9.2% for MxH plants originating also from vitroplants. On the contrary, no apparent differential activation was registered for infectious allele OL1 at 15 months after planting, regardless of the nature of the planting material and the variety. Although

these results are still preliminary, they suggest that by the end of the assay, the proportion of BSOLV and BSGFV infections

resulting from the activation of infectious alleles OL1 and GF7 is likely to differ between varieties and within varieties depending on the mode of multiplication of the planting material.

The second compound of the risk of spreading BSOLV and BSGFV (the impact of BSV infection on production) was also monitored in the assay. Considering the low number of infected plants at bunch harvest time, results could not be statistically supported, precluding definite conclusions. However, only 5/16 (31.25%) of infected plants displayed BSV-like symptoms and only limited impact on plant growth and fruit production was measured. These observations correlate with those made also on FHIA-2A and MxH during the above mentioned surveys: BSV-like symptoms were observed only on a limited number of MxH and FHIA-21 plants, and their correlation with positive indexing results was poor; most BSV-infected plants were symptomless, suggesting that BSOLV and BSGFV infections had a very limited impact on plants and production –if any-.

IV-3. Towards a global strategy for the control the deleterious effects of infectious eBSVs

This thesis brings a significant contribution to the implementation of a global strategy for the control of the deleterious effects of infectious eBSVs in interspecific hybrids. While a new generation of *M. balbisiana* genitors free of infectious eBSVs is being developed (Umber *et al.*, submitted) for breeding novel interspecific hybrids with no risk of activating infectious eBSVs, the work described in this thesis paves the way to a proper quantification of this risk in existing interspecific hybrids which *do* carry infectious eBSVs. The methodology that was developed in this work allows similar evaluation programs to be carried out for other interspecific hybrids. This is the case in Cuba and in Guadeloupe where identical field experiments are being carried out in order to quantify the risk of spreading BSVs through the cultivation of other interspecific hybrids and varieties (FHIA-18, Pelipita, and French Clair) that are widely cultivated in these countries and territories. The results of these evaluation programs will make it possible to develop and implement appropriate strategies for mitigating risks.



CHAPTER V

MATERIALS & METHODS

V-1. Field surveys and collection of samples

A nationwide survey was carried out in order to assess the prevalence and diversity of BSV species BSOLV, BSGFV and BSIMV in interspecific hybrids in the Dominican Republic. To this aim, leaf samples of interspecific hybrids FHIA-21 (AAAB) and Macho X Hembra (AAB) were randomly collected between January 2012 and July 2013 from 36 plantations distributed across all 5 banana producing regions located in 11 of the 31 Dominican provinces and representing the diversity of environments and agronomic practices encountered in banana growing areas throughout the country. Figure II-1 shows the location of collection sites. 8-13 leaf samples (ca 1cm²) were collected on each site to a total of 590 samples including 299 samples from MxH and 291 samples from FHIA-21. Samples were labelled, wrapped in wet paper towels, placed in plastic bags and transported in a cooler until stored at 4°C in the laboratory until processing, with storage time never exceeding one week. For each sampled plant, data including crop growth cycle, source of planting material (vitroplant or sucker), presence and nature of an irrigation system, presence or absence of mealybugs, BSV or Black Sigatoka symptoms were recorded. Data on weather and environmental conditions of the sampled plots were gathered from the Dominican weather bureau (*Oficina Nacional Meteorología, ONAMET*).

An in-depth survey was carried out in October 2013 on larger sample counts from 2 locations, Monte Christi and Puerto Plata. In both locations, 100 leaf samples were collected randomly from FHIA21 and from MxH plants grown on adjoining plots, leading to a total of 400 collected samples. The presence of BSV symptoms and mealybug counts were recorded for each sampled plant.

An additional 248 leaf samples of Cavendish dessert banana (AAA) were collected between February and April 2014 from 12 plantations distributed over 5 provinces as described above.

V-2. BSV indexing by multiplex immunocapture PCR (M-IC-PCR)

Collected leaf samples were indexed for the presence of BSV species BSOLV, BSGFV, and BSIMV by multiplex immunocapture PCR (M-IC-PCR), according to Le Provost *et al.* (2006) with modifications. A rabbit polyclonal antiserum kindly provided by B.E.L. Lockhart (University of Minnesota, USA) was used for the immunocapture step. This antiserum has the ability to detect a wide range of badnaviruses, including most BSV species (Ndowora, 1998; Ndowora and Lockhart, 2000). 96-well microtiter plates (Agdia, Madison WI, USA) were coated overnight at 4°C with 25 µl of IgG, purified from the antiserum and diluted at 2 µg/ml in coating carbonate buffer (15 mM sodium carbonate, 34 mM sodium bicarbonate, pH 9.6), then washed three times with 100 µl of PBT washing buffer (136 mM NaCl, 1.4 mM KH₂PO₄, 2.6 mM KCl, 8 mM NA₂HPO₄, 0.05% Tween-20, pH 7.4).

Crude extracts were prepared in meshed plastic bags (Agdia, Madison, WI, USA) by grinding 0.5 g of collected leaf samples or 0.05g of lyophilized leaf material in 5 ml of grinding buffer (2% polyvinylpyrrolidone 40, 0.2% sodium sulfite and 0.2% bovine serumalbumine, prepared in PBT), using a bead grinder, then transferred to

microfuge tubes. When using lyophilized leaf material, 0.05 g were ground in 5 mL of grinding buffer. Extracts were clarified by centrifugation at 8,000 rpm for 2 min at room temperature, and 25 µL of supernatant was deposited in the antibody pre-coated wells of the microtiter plates for the immunocapture step. Plates were incubated for 30 min at room temperature, then rinsed four times with 100 µL of PBS-T and twice with ultrapure sterile water (Roth, Karlsruhe, Germany).

A DNase I treatment was performed on samples following the immunocapture step and before the PCR step in order to eliminate plant genomic DNA and prevent false positives that could result from the amplification of eBSV sequences. To this end, samples were treated with 2 U of RQ1 DNase (Promega, Charbonnières, France) as described by Gambley (2008). Following heat denaturation of RQ1 DNase (10 min at 95°C), separate PCR amplifications were performed for each BSV species by adding 25 µL of PCR mix in each well. PCR mix contained 2.5 µL of 10x reaction buffer (400 mM Tris-HCl pH 8, 100 mM MgSO₄, 10 mM CaCl₂), 0.75 µL of 50 mM MgCl₂, 2 µL of 2.5 mM dNTPs, 1 U of Taq DNA polymerase (New England Biolabs, Evry, France), either 1 µL of 2 µM forward and reverse BSGFV-specific primers, 0.75 µL of 2 µM forward and reverse BSOLV-specific primers or 0.5 µL of 2 µM forward and reverse BSGFV-specific primers and 0.75 µL of 2 µM forward and reverse Monkey transposon-specific primers. Primer sequences are provided in Table II-1.

PCR conditions were an initial denaturation step at 94°C for 5 min, followed by 35 cycles of 30s at 94°C, 30 s at 58°C, 30s at 72°C and one cycle of 10 min at 72°C. Ten µL of reaction mixes were analysed by electrophoresis on a 1% agarose gel prepared in 0.5xTBE (45 mM Tris-borate, 1 mM EDTA, pH 8.0) containing 0.005% of GelRed (Biotium, Hayward, USA). Amplification products were visualized and photographed under UV light.

Table V-1. Nucleotide sequences of the primers used in M-IC-PCR experiments

Target	Primer name	Primer sequence (5'-3')	Expected size of PCR product	Reference
BSOLV	RD-F1	ATCTGAAGGTGTGTTGATCAATGC	522	Geering <i>et al.</i> , 2000
	RD-R1	GCTCACTCCGCATCTTATCAGTC		
BSGFV	GF-F1	ACGAACTATCACGACTTGTTCAAGC	476	
	GF-R1	TCGGTGGAATAGTCCTGAGTCTTC		
BSIMV	IM-F1	CACCCAGACTTTTCTTTCTAG C	384	Geering <i>et al.</i> , 2014
	IM-R1	TGCCAACGAATACTACATCAAC		
Monkey	MonF2	GTC GAC ACA TGG GAG GAC TT	300	Gambley, 2008
	MonR2	CTT GTT GGG TCT TCA GAG GAA		

V-3. Extraction and quality check of banana genomic DNA

Total genomic DNA was extracted from leaf samples using the Plant DNeasy minikit (Qiagen, Courtaboeuf, France). The quality of DNA was assessed by electrophoresis as described above, by loading 1 µL of DNA solution, and by PCR using primers targeting the actin gene (Actine1F : 5'-TCC TTT CGC TCT ATG CCA GT-3'; Actine1R : 5'-GCC CAT CGG GAA GTT CAT AG-3'). PCR mix contained 1 µL of purified genomic DNA, 2,5 µL of 10x reaction buffer (400 mM Tris-HCl pH 8, 100 mM MgSO₄, 10 mM CaCl₂), 0,75 µL of 50 mM MgCl₂, 2 µL of

2.5 mM dNTPs, 1 U of Taq DNA polymerase (New England Biolabs, Evry, France), 1 µL of each primer and ultrapure sterile water to 25 µL. PCR conditions were an initial denaturation step at 94°C for 5 min, followed by 25 cycles of 30s at 94°C, 30s at 58°C, 1 min at 72°C and one cycle of 10 min at 72°C. Electrophoresis analyses of amplification products were performed as described above.

V-4. eBSV genotyping

eBSOLV, eBSGFV and eBSIMV patterns were assessed by PCR-based screening on a selection of 49 symptomless sampled FHIA21 and MxH hybrids, using the PCR and dCAPS (derived cleaved amplified polymorphic sequences) primers and conditions described by Gayral *et al.* (2008) and Chabannes *et al.* (2013). The list and sequence of primers used are provided in Table II-2. Three types of primers were used: they are specific of eBSV / *Musa* junctions, eBSV internal structure or allelic forms, respectively, as illustrated on Figure V-2.

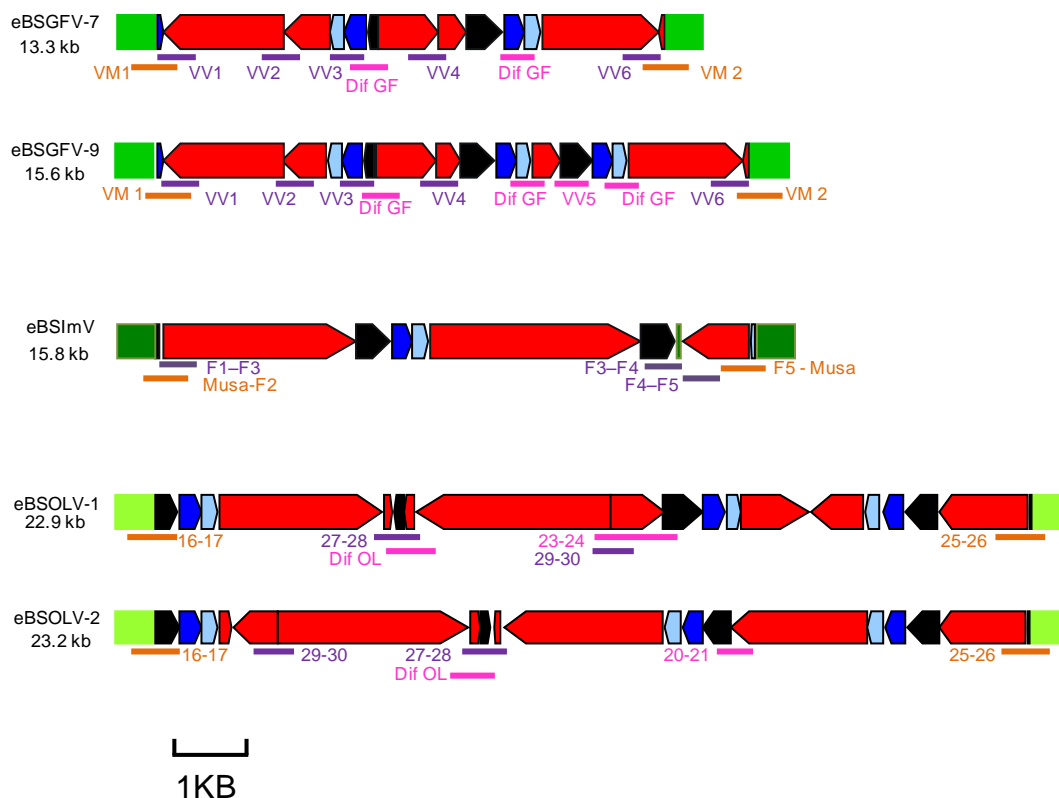


Figure V-1: location of the PCR and dCAPS specific primers on the corresponding eBSVs in model species PKW.

PCR products amplified using primers specific of eBSV / *Musa* junctions, eBSV internal structure or allelic forms are shown by orange, purple and pink lines, respectively.

From Baurens *et al.*, 2013; Duroy, 2014.

Table V-2. PCR and dCAPS specific markers used to genotype eBSVs (from Chabannes *et al.*, 2013 ; Duroy, 2014)

Target	Type of markers	Primer name	Primer sequence (5'—3')	Size of PCR product (bp)
eBSGFV	Integration locus	VM1F	TTGTCCAAAATCTGCTCGTG	481
		VM1R	TGTAATTCCTGCTCCTGCAA	
		VM2F	TTCTCCCTTTTCGATCCGTA	374
		VM2R	TTTTGATGCATCTCCAGCAG	
	Structure	VV1F	ACAGCTCCAGGAGATTGGAA	268
		VV1R	CTGAAGTGTGCCTGTGGAGA	
		VV2F	TCTGAGATCTCCAGCCAGGT	639
		VV2R	GACAGTTCAGCACAGCAGA	
		VV3F	TTGCCAAGAATTCCTCAAG	376
		VV3R	AAGTTCCTGTCGGCAAGGTG	
		VV4F	GAGCAACACGAGTCAACGAA	784
		VV4R	TCTCCACAGGCACACTTCAG	
	Allelic	VV6F	GCATGAAGCATGACTGGAGA	264
		VV6R	AATGCATAAGGGCCTCGAAT	
		VV5F	CCATGGAGGTTGACCTGTCT	628
		VV5R	ACCCCTCTGTCTTCCAACT	
		DifGfF	TTGCAGGAGCAGGAATTACA	670
		DifGfR	GGATGGAAGATGAGCTCTTTG	
eBSOLV	Integration locus	Musa-OL jonction1 F	TGCATTAGATGGTCTGGGAAA	563
		Musa-OL jonction1 R	ACTTCACGATGCCCATGTTT	
		Musa-OL jonction2 F	GAGCTGTTTCCTCCGTGTCT	590
		Musa-OL jonction2 R	CCTGGAAGAAAGCAGACGAG	
	Structure	sig1 eBSOLV F	TTCGAGGAGTCAACGGAGTC	606
		sig1 eBSOLV R	CCTGGTCTGCACAGAGATGA	
		sig2 eBSOLV F	CTTGCTCTGTGGGCAAGACT	426
		sig2 eBSOLV R	CCATTTTCTCGCAGATTGTC	
	Allelic	Marker1-BSOLV(2) F	ATACGAAGCCCAACGAATTG	601
		Marker1-BSOLV(2) R	ATGGCTTGCTTCACAGATT	
		Marker2-BSOLV(2) F	ACTCGCACAAGTGAACGTCG	399
		Marker2-BSOLV(2) R	ACAGTACAAGCCCCACCAAT	
		Marker2-BSOLV(1) F	GTGGTGGTCTTGATCCGGT	1469
		Marker2-BSOLV(1) R	CACGTGGTAGGGGTCCGCCA	
		Dif-OL(F) (HaeIII)	GAATCATTATTCGAGGAGTCAACGG	337
		Dif-OL(R) (HaeIII)	CGAGTAGAGCGCAAGATCCTAGTTC	
SimV	Integration locus	Dif-OL (F) (AhdI)	TTGGAACAAGACAGATTGACTTCCT	500
		Dif-OL (R) (AhdI)	GGTTCGTTTTATGGCTTTCATGG	
	Structure	Musa/F2-F	ACTCAGCAAAGGCAAGCAGT	561
		Musa/F2-R	TCTGGTGTGAGTTTTAATAATACCG	
		F5/Musa-F	GTATGGTTCTTGCCCGATGA	594
		F5/Musa-R	TCGTGCAGACCCCTTACTCT	
	Allelic	F1/F3-F	TTCGGTATTATTAATAACTCACACCA	490
		F1/F3-R	GCTGCTAACTGAGGATAATCGAA	
		F3/F4-F	TCCCACGCAAGCTTACTTCT	600
		F3/F4-R	GAAGCTGTCCAAGCCTATATCA	
		F4/F5-F	TGGACAGCTTCTGGTGTGAG	540
		F4/F5-R	AGCAGCTACAACCTGGAGA	

PCR mix contained 2.5 µL of genomic DNA, 2.5 µL of 10x reaction buffer (400 mM Tris-HCl pH 8, 100 mM MgSO₄, 10 mM CaCl₂), 1.5 µL of 50 mM MgCl₂, 1 µL of 2.5mM dNTPs, 1 U of Taq DNA polymerase (New England Biolabs, Evry, France), 2.5 µL of forward and reverse primers at 2.5mM each and ultrapure sterile water to 25 µL.

PCR conditions differed depending on primers:

- for eBSGFV- and eBSImV- specific primers, they were an initial denaturation step at 94°C for 5 min, followed by 25 cycles of 30s at 94°C, 30 s at 58°C, 1min at 72°C and one cycle of 10min at 72°C
- for eBSOLV-specific primers, they were an initial denaturation step at 94°C for 5 min, followed by 30 cycles of 30s at 94°C, 30 s at 65°C, 1min at 72°C and one cycle of 10min at 72°C
- for the DigGF/DigGR primer couple, they were an initial denaturation step at 94°C for 5 min, followed by 35 cycles of 30s at 94°C, 30 s at 55°C, 30s at 72°C and one cycle of 10min at 72°C. In that specific case, an aliquot of 7 µL of the amplification products was digested overnight by 1 U of restriction enzyme HpyCH4 III (New England Biolabs, Evry, France), an isochisomer of restriction enzyme Taal, prior to electrophoresis. Expected digestion products three fragments of 442 bp, 227 bp and 76 bp for eBSGF9 and two fragments of 366 bp, 227 bp for eBSGF7, respectively.

Electrophoresis analyses of amplification products were performed as described above. eBSV patterns were compared to reference patterns of model species PKW (Gayral *et al.* 2008; Chabannes *et al.* 2013).

V-5. Molecular characterization of mealybugs

A total of 400 mealybugs at various developmental stages were collected from the pseudostem of plants sampled in Montecristi and Puerto Plata during the in-depth BSV survey (see above). Plants displayed various infestation levels; some were heavily infested whereas others were not infested at all. Therefore, several insects were collected on heavily infested plants whereas none were collected from mealybug-free plants. Insects were immediately placed in microfuge tubes containing 70% alcohol upon collection and kept at room temperature or at -20°C until further use.

Each collected insect was dried, placed at -80°C for 30 min in a 2 ml Safe Lock microfuge tube (Eppendorf, Montesson, France) with a 5mm steel bead (Loudet Industries, St Jean de Vedas, France) and ground in 150 µL of PBS (137 mM NaCl, 2, 7 mM KCl, 10 mM Na₂HPO₄, 1,76 mM KH₂PO₄) using a Tissue Lyzer (Qiagen, Courtaboeuf, France). Total genomic DNA was extracted from each insect using the NucleoSpin® 96 Virus Core Kit (Macherey Nagel, Hoerd, France) and the automated extraction station Biomek 4000 (Beckman Coulters, Villepinte, France). Purified DNA was eluted in 200 µL of ultra-pure water.

Molecular characterization of mealybugs was carried out by PCR, using the primers listed in Table II-3. Universal primers C1-J-2183 and TL2-N- 3014 (Simon *et al.*, 1994) were used to amplify a 831 bp fragment in a highly conserved region of the gene encoding mitochondrial cytochrome c oxidase subunit 1 (COI).

Specific identification of species *Planococcus citri*, *Planococcus ficus*, *Pseudococcus longispinus*, *Planococcus minor* and *Dysmicoccus brevipes* was also attempted by PCR, using species-specific primers:

- For *P. citri*, *P. ficus* and *P. longispinus*, primer TL2N-3014 (Simon *et al.*, 19894) was used in a multiplex assay (Saccagi *et al.*, 2008) with primers C1-J-2260, C1-J-2427 and C1-J-2608 (Simon *et al.*, 1994). PCR conditions were an initial denaturation step at 94°C for 4 min, then 35 cycles of 1min at 94°C, 1min at 51°C, 1.5min at 72°C and one cycle of 72°C for 4 min.
- For *P. minor*, primer couple C1-J-2183 / 3014-R2 (Rung *et al.* 2009) was used. PCR conditions were an initial denaturation step at 94°C for 5 min, then 35 cycles of 45s at 94°C, 45s at 48°C, 1 min at 72°C and one cycle of 72°C for 10 min.
- For *Dysmicoccus brevipes* primer couple Dybr and Dybf was used (Simon *et al.*, 1994). PCR conditions were an initial denaturation step at 95°C for 30s, then 35 cycles of 45s at 95°C, 45s at 61°C, 1min at 72°C and one cycle of 72°C for 5 min.

PCR mixes contained 1 µl of extracted DNA diluted 1:10, 2.5 µl of each forward and reverse primer at 2.5mM, 2, 5 µl of 10x reaction buffer (400 mM Tris-HCl pH 8, 100 mM MgSO₄, 10 mM CaCl₂), 2 µl of 50 mM MgCl₂, 0.5 µl of 2.5mM dNTPs, 1 U Taq polymerase (New England Biolabs, Evry, France), and nuclease free water up to a final volume of 25 µl. min

Following analyses by electrophoresis as described above, amplification products were purified using the Qiaquick PCR purification kit (Qiagen, Courtaubeuf, France) and sequenced by Beckman Coulter Genomics (Takeley, UK). A phylogenetic tree was built with MEGA6 using the Neighbor-Joining method based on the HKY model (Hasegawa *et al.*, 1985; Tamura *et al.*, 2011). Alignments were performed using CLUSTALW (Larkin *et al.*, 2007).

Table V-3. Nucleotide sequences of the primers used for the molecular characterization of mealybugs

Target	Primer pair	Primer sequence (5'-3')	Expected size of PCR product (bp)	Reference
Generic	TL2-N-3014	TCCAATGCACTAATCTGCCATATTA	831 bp	Simon <i>et al.</i> , 1994
	CJ-J-2183	CAACATTATTTTGATTTTTGGN		
<i>P. minor</i>	CJ-J-2183	CAACATTATTTTGATTTTTGGN	840	Rung <i>et al.</i> , 2009
	3014-R2	AATGTATGATTTAAATTAGGTG		
<i>P. ficus</i>	C1-J-2260	TCAAATTATAAATCAAGAAAGGGGAAAC	754	Simon <i>et al.</i> , 1994; Sacagi <i>et al.</i> , 2008
	TL2-N-3014/	TCCAATGCACTAATCTGCCATATTA		
<i>P. citri</i>	C1-J-2427	TAATTATTGCTATTCTACAAGAATTAATC	587	Simon <i>et al.</i> , 1994; Sacagi <i>et al.</i> , 2008
	TL2-N-3014/	TCCAATGCACTAATCTGCCATATTA		
<i>P. citri</i>	CitriFor1	5'-CAGGTGGAACACTTTACCCTCCT-3'	700	Rung <i>et al.</i> , 2009
	CitriRev1	5'-AATTGCTCTTGATAAAATTGGAA-3'		
<i>P. longispinus</i>	C1-J-2608	TTTGTGTAGCACATTTTCATTATGTAC	406	Simon <i>et al.</i> , 1994; Sacagi <i>et al.</i> , 2008
	TL2-N-3014	TCCAATGCACTAATCTGCCATATTA		
<i>D. brevipes</i>	Dyb-1F	ATAAATCAAGAAAGAGGTAAATTAG	742	Simon <i>et al.</i> , 1994
	Dyb-1R	TTAGGATTATTATTAATTCATTAG		

V-6. Assessment of the activation rates of infectious eBSVs in FHIA-21 and MxH hybrids under field conditions

A field experiment was established in Barranca (La Vega) in March 2013 in order to compare the levels of expression of infectious eBSVs in hybrids FHIA 21 and MxH in plants originating from tissue culture (vitroplants) and from suckers and to measure the impact of BSV infection on fruit production for those hybrids. Negative controls were plants from the Williams variety, whose AAA genome is free of any eBSV.

V-6.1. Production of planting material

Vitroplants and suckers were used as planting material. Vitroplants were obtained from CENTA (Centro de Tecnologías Agrícolas, Santo Domingo, Dominican Republic) using meristem culture according to Côte *et al.* (1990). Suckers were produced at IDIAF experimental station of Centro Norte at La Vega. Rooted plantlets and suckers were individually transferred to plastic bags filled with fertilized soil Nitrogen- Phosphorus-Potassium (NPK) fertilizer (Basfoliar, Compo Agro, Santo Domingo) and hardened in an insect proof greenhouse for two months. At the end of this period, all plants were fully indexed by ELISA for CMV and BBTv using diagnostic kits and protocols from Agdia (Biofords, Evry, France), by immunocapture reverse transcriptase PCR for BBtMV according to Iskra Caruana *et al.* (2008), for BanMMV according to Teycheney *et al.* (2007b) and by M-IC-PCR for BSOLV, BSGFV and BSIMV as described above. Infected plants were discarded and only healthy plants were used as planting material.

V-6.2. Design of the field experiment

The experiment consisted in 80 complete randomized blocks (see Figure III-1), each comprising 5 distinct types of planting material arranged in a random fashion (one single plant per elementary plot), that were further considered as distinct statistical treatments (numbered T1 to T5):

- T1: MxH vitroplants
- T2: MxH suckers
- T3: FHIA21 vitroplants
- T4: FHIA21 suckers
- T5: Williams vitroplants

Williams plants (AAA genotype) originating from vitroplants were also used as an outer border (84 plants) in order to monitor external mealybug-mediated contaminations of the experiment. Distance between plants was 2m and total surface of the experiment was 0.23 ha, leading to an overall plant density of 2100 plants/ha. Figure II-3 below shows the organization of the field experiment.

V-6.3. Maintenance of the experimental plot

Ants move mealybugs from plant to plant and play a key role in mealybug-mediated disease transmission. In order to prevent BSV transmission by mealybugs, ants were controlled by weekly applications of Diazinon 60 EC diluted to 6.25 g/ L (Shanghai Bosman Industrial Co., Ltd., Shanghai, China) and Carbosulfan diluted to 7.5 g/ L (Sikko Industries Ltd., Vejalpur Ahmedabad, India).

Fertilization plan was as follows: an initial application of 113.3 g of a potassium nitrate / magnesium mix was performed on each plant one month after planting, and then five applications of 2 g of this mix were performed per plant through the crop cycle.

Black Sigatoka was controlled by regular defoliation of symptomatic leaves and alternated manual applications of Bankit 25 SC diluted at 50 cL/ha (Syngenta, Cambridge, UK), Tilt 25 EC diluted at 50 cL/ha (Syngenta, Cambridge, UK) or Indar 25 OF diluted at 40 cL /ha (Dow AgroSciences, Jalisco, México), mixed with 4 l/ha of mineral oil used as an adjuvant (COSMO OIL® 80 EO, Shibaura, Minato-ku, Japan). Weed control was performed manually once a week and by bi-monthly applications of 1 L/ha of Glyphosate (*Roundup*®, Monsanto, St Louis, USA) and 1.5 L/ha of Paraquat (*Gramoxone*®, Syngenta, Cambridge, UK). At 7 months after planting, one sucker was selected to serve as daughter plants (ratoon crops) for the second cycle, and the other suckers were eliminated by cutting. The sanitary status of the plot was evaluated by visual inspections every three weeks during the first cycle and monthly during the second cycle.

V-6.4. Sample collection, evaluation and viral indexing

Leaf samples were collected every three months after planting and indexed for BSOLV, BSGFV and BSIMV, as described above (see V-2.). Plants found infected by any of these viruses were left on the plot.

At the end of the first cycle, bunches were harvested from all (infected and non-infected) plants of the plot and evaluated for the following criteria:

- Plant height
- Pseudostem girth
- Bunch weight
- Number of hands per bunch
- Number of fingers per bunch
- Average finger diameter
- Average fingers length

V-7. Statistical analyses

The experimental treatment structure allows a 2x2 factorial analysis of the data by crossing the variety factor (MxH and FHIA-21) and the multiplication mode factor (vitroplant and sucker). Comparisons of activation rates of infectious eBSVs were performed using the Glimmix procedure of SAS (SAS 9.3 software, 2002-2010, SAS Institute Inc., Cary, NC, USA) which fits generalized linear mixed model and allows logistic regression. Because of several blocks having a mean equal to zero, block factor was considered as random.

Dotplots showing the distribution of individual agronomical parameters were generated using the Minitab 15 software (Minitab Inc, State College, Pennsylvania, USA).

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Annexes

Annexes

Annex 1: Full indexing results for the FHIA-21 samples collected during the nationwide survey

Sample	Sampling location		GPS coordinates			Plot superfcy (ha)	Planting material	Origin of plants	Age of plot (year)	Plant density (p/ha)	Irrigation	type d'irrigation	Crop association	Weed control	Banana surrounding	Sigatoka control	BSV symptoms on plot	Sigatoka severity index	Mealybugs on the plot	indexations		
	Province	Municipality	Longitude (west)	Latitude (north)	Altitude (m)															BSOLV	BSGFV	BSIMV
1	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	0	0
2	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	0	0
3	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	1	1	0
4	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	0	0
5	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	1	0
6	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	0	0
7	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	1	0
8	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	0	0
9	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	1	0
10	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	1	0
11	Montecristi	Jaramillo	WO 71° 37,764'	N 19°47,269'	20	40	sucker	Dom Rep	4	2800	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,753	Yes	0	0	0
12	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	0	0	0
13	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	1	0	0
14	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	0	0	0
15	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	0	0	0
16	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	0	1	0
17	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	0	0	0
18	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	0	0	0
19	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	1	1	0
20	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	0	0	0
21	Montecristi	Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	Yes	6,316	Yes	1	0	0
22	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	0	0	0
23	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	0	1	0
24	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	1	0	0
25	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	0	0	0
26	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	1	0	0
27	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	0	0	0
28	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	0	0	0
29	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	1	1	0
30	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	1	0	0
31	Puerto Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	9,4	sucker	Dom Rep	3	3179	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	8,409	Yes	1	0	0
32	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	0	0	0
33	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	0	1	0
34	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	1	1	0
35	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	0	0	0
36	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	1	0	0
37	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	0	0	0
38	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	1	0	0
39	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	0	0	0
40	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	0	1	0
41	Puerto Plata	Bellosio	WO 71° 01,018'	N 19° 50,173'	25	12	sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	Yes	9,754	Yes	0	0	0
42	Valverde Mao	Sabana Grande	WO 71° 03,948'	N 19° 31,9373'	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	0	0	0

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43	Valverde Mao	Sabana Grande	WO 71° 03,949	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	0	0	0
44	Valverde Mao	Sabana Grande	WO 71° 03,950	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	1	0	0
45	Valverde Mao	Sabana Grande	WO 71° 03,951	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	0	1	0
46	Valverde Mao	Sabana Grande	WO 71° 03,952	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	0	0	0
47	Valverde Mao	Sabana Grande	WO 71° 03,953	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	1	0	0
48	Valverde Mao	Sabana Grande	WO 71° 03,954	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	0	1	0
49	Valverde Mao	Sabana Grande	WO 71° 03,955	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	0	0	0
50	Valverde Mao	Sabana Grande	WO 71° 03,956	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	0	1	0
51	Valverde Mao	Sabana Grande	WO 71° 03,957	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	0	0	0
52	Valverde Mao	Sabana Grande	WO 71° 03,957	N 19° 31,937'3	84	8,8	sucker	Dom Rep	1,5	3000	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,389	Yes	0	0	0
53	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	0	1	0
54	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	0	0	0
55	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	1	0	0
56	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	0	0	0
57	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	0	0	0
58	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	0	1	0
59	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	1	1	0
60	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	1	0	0
61	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	0	0	0
62	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	0	0	0
63	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	0	0	0
64	Valverde Mao	Boca de Mao	WO 71° 02,755	N 19° 35,420'	73	0,3	sucker	Dom Rep	2	3179	Yes	Inundation	No	Manual	No	Mixed	No	7,07	Yes	0	0	0
65	Valverde Mao	Esperanza	WO 71° 00,202	N 19° 34,908'	100	0,9	sucker	Dom Rep	3	2861	Yes	Inundation	Yes	Manual	Yes	Deleafing	Yes	3,2				

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95	Santiago-Banegas1	Banegas 1	WO 70° 47,787'	N 19° 31,838'	144	2	sucker	Dom Rep	1,5	2700	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	7,788	No	0	0	0	0
96	Santiago-Banegas1	Banegas 1	WO 70° 47,787'	N 19° 31,838'	144	2	sucker	Dom Rep	1,5	2700	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	7,788	No	0	0	0	0
97	Santiago-Banegas1	Banegas 1	WO 70° 47,787'	N 19° 31,838'	144	2	sucker	Dom Rep	1,5	2700	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	7,788	No	0	0	0	0
98	Santiago-Banegas 2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	1	0	0
99	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	0	0	0
100	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	0	0	0
101	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	0	0	0
102	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	1	0	0
103	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	0	0	0
104	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	0	0	0
105	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	1	0	0
106	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	0	0	0
107	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	1	0	0	0
108	Santiago-Banegas2	Banegas 2	WO 70° 47,304'	N 19° 32,038'	154	7,8	sucker	Dom Rep	3	3815	Yes	Inundation	No	Herbicide	Yes	Mixed	Yes	6,638	No	0	1	0	0
109	Santiago-Hatillo	San Lorenzo1	WO 70° 50,616'	N 19° 29,580'	159	3,7	sucker	Dom Rep	1,6	3179	Yes	Dripping	No	Mixed	Yes	Deleafing	Yes	6,273	Yes	1	0	0	0
110	Santiago-Hatillo	San Lorenzo1	WO 70° 50,616'	N 19° 29,580'	159	3,7	sucker	Dom Rep	1,6	3179	Yes	Dripping	No	Mixed	Yes	Deleafing	Yes	6,273	Yes	0	0	0	0
111	Santiago-Hatillo	San Lorenzo1	WO 70° 50,616'	N 19° 29,580'	159	3,7	sucker	Dom Rep	1,6	3179	Yes	Dripping	No	Mixed	Yes	Deleafing	Yes	6,273	Yes	0	1	0	0
112	Santiago-Hatillo	San Lorenzo1	WO 70° 50,616'	N 19° 29,580'	159	3,7	sucker	Dom Rep	1,6	3179	Yes	Dripping	No	Mixed	Yes	Deleafing	Yes	6,273	Yes	0	0	0	0
113	Santiago-Hatillo	San Lorenzo1	WO 70° 50,616'	N 19° 29,580'	159	3,7	sucker	Dom Rep	1,6	3179	Yes	Dripping	No	Mixed	Yes	Deleafing	Yes	6,273	Yes	0	0	0	0
114	Santiago-Hatillo	San Lorenzo1	WO 70° 50,616'	N 19° 29,580'	159	3,7	sucker	Dom Rep	1,6	3179	Yes	Dripping	No	Mixed	Yes	Deleafing	Yes	6,273	Yes	0	1	0	0
115	Santiago-Hatillo	San Lorenzo1	WO 70° 50,616'	N 19° 29,580'	159	3,7	sucker	Dom Rep	1,6	3179	Yes	Dripping	No	Mixed	Yes	Deleafing	Yes	6,273	Yes	0	0	0	0
116	Santiago-Hatillo	San Lorenzo1	WO 70° 50,616'	N 19° 29,580'	159	3,7	sucker</																

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147	Hermanas Mirabal	Celba 1	WO 70° 25,351'	N 19° 19,286'	133	1,25	sucker	Other	8	1589	No	None	No	Herbicide	Yes	Deleafing	Yes	10,241	Yes	0	0	0
148	Hermanas Mirabal	Celba 1	WO 70° 25,351'	N 19° 19,286'	133	1,25	sucker	Other	8	1589	No	None	No	Herbicide	Yes	Deleafing	Yes	10,241	Yes	0	1	0
149	Hermanas Mirabal	Celba 1	WO 70° 25,351'	N 19° 19,286'	133	1,25	sucker	Other	8	1589	No	None	No	Herbicide	Yes	Deleafing	Yes	10,241	Yes	0	0	0
150	Hermanas Mirabal	Celba 1	WO 70° 25,351'	N 19° 19,286'	133	1,25	sucker	Other	8	1589	No	None	No	Herbicide	Yes	Deleafing	Yes	10,241	Yes	0	0	0
151	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	0	0	0
152	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	0	0	0
153	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	0	0	0
154	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	0	0	0
155	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	0	0	0
156	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	0	1	0
157	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	0	0	0
158	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	0	0	0
159	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	0	0	0
160	Hermanas Mirabal	Celba 2	WO 70° 25,060'	N 19° 19,802'	147	0,8	sucker	Dom Rep	9	1589	No	None	Yes	Mixed	Yes	Fungicide	No	12,132	Yes	1	0	0
161	Hermanas Mirabal	Celba 3	WO 70° 25,394'	N 19° 19,962'	148	15	sucker	Dom Rep	3	2157	No	None	No	Mixed	Yes	Fungicide	Yes	10,681	Yes	0	0	0
162	Hermanas Mirabal	Celba 3	WO 70° 25,394'	N 19° 19,962'	148	15	sucker	Dom Rep	3	2157	No	None	No	Mixed	Yes	Fungicide	Yes	10,681	Yes	0	0	0
163	Hermanas Mirabal	Celba 3	WO 70° 25,394'	N 19° 19,962'	148	15	sucker	Dom Rep	3	2157	No	None	No	Mixed	Yes	Fungicide	Yes	10,681	Yes	0	0	0
164	Hermanas Mirabal	Celba 3	WO 70° 25,394'	N 19° 19,962'	148	15	sucker	Dom Rep	3	2157	No	None	No	Mixed	Yes	Fungicide	Yes	10,681	Yes	0	0	0
165	Hermanas Mirabal	Celba 3	WO 70° 25,394'	N 19° 19,962'	148	15	sucker	Dom Rep	3	2157	No	None	No	Mixed	Yes	Fungicide	Yes	10,681	Yes	1	0	0
166	Hermanas Mirabal	Celba 3	WO 70° 25,394'	N 19° 19,962'	148	15	sucker	Dom Rep	3	2157	No	None	No	Mixed	Yes	Fungicide	Yes	10,681	Yes	0	0	0
167	Hermanas Mirabal	Celba 3	WO 70° 25,394'	N 19° 19,962'	148	15	sucker	Dom Rep	3	2157	No	None	No	Mixed	Yes	Fungicide	Yes	10,681	Yes	0	1	0
168	Hermanas Mirabal	Celba 3	WO 70° 25,394'	N 19° 19,962'	148	15	sucker	Dom Rep	3	2157	No	None	No	Mixed	Yes	Fungicide	Yes	10,681	Yes	0	0	0
169	Hermanas Mirabal	Celba 3	WO 70° 25,394'	N 19° 19,962'	1																	

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199	Espaillat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	5,4	sucker	Dom Rep	9	2305	No	None	No	Mixed	Yes	Fungicide	Yes	15,152	Yes	0	0	0
200	Espaillat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	5,4	sucker	Dom Rep	9	2305	No	None	No	Mixed	Yes	Fungicide	Yes	15,152	Yes	0	0	0
201	Espaillat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	5,4	sucker	Dom Rep	9	2305	No	None	No	Mixed	Yes	Fungicide	Yes	15,152	Yes	0	0	0
202	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	0	1	0
203	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	0	0	0
204	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	0	1	0
205	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	1	0	0
206	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	0	0	0
207	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	0	0	0
208	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	1	1	0
209	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	0	1	0
210	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	0	0	0
211	La Vega	Jamo	W70°32.032'	N19°13, 234'	97	5	sucker	Dom Rep	1,5	2000	No	None	No	Mixed	Yes	Mixed	Yes	24,734	Yes	1	0	0
212	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	0	0	0
213	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	0	0	0
214	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	0	0	0
215	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	1	0	0
216	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	0	0	0
217	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	0	0	0
218	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	0	0	0
219	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	1	0	0
220	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	0	0	0
221	La Vega	Barranca 1	WO 70° 26,890'	N 19° 16,610'	108	25	sucker	Dom Rep	3	2000	No	None	No	Herbicide	Yes	Fungicide	Yes	8,214	Yes	0	0	0
222</																						

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Contribution to the assessment of the risk of spreading banana streak viruses (BSVs) in the Dominican Republic through the cultivation of banana interspecific hybrids harbouring infectious endogenous BSV sequences.

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251	La Vega	Barranca 4	WO 70° 27,560'	N 19° 15,576'	107	2,8	sucker	Dom Rep	1	1987	No	None	No	Herbicide	Yes	Deleafing	No	6,742	Yes	0	0	0
252	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
253	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
254	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	0	1	0
255	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	0	1	0
256	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
257	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	0	1	0
258	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	1	1	0
259	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
260	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	0	1	0
261	Monteplata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	6,3	sucker	Dom Rep	9	2500	Yes	Unknown	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
262	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
263	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
264	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
265	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
266	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	1	0
267	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
268	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
269	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
270	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
271	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	1	0
272	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	9,7	sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
273	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	0	0	0
274	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	0	0	0
275	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	0	0	0
276	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	0	0	0
277	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	0	0	0
278	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	0	0	0
279	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	0	0	0
280	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	0	0	0
281	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	1	0	0
282	San Juan	Pajonal	WO71°23, 332'	N 18°80, 213'	415	4,2	sucker	Dom Rep	6	1100	No	None	No	Mixed	Yes	Mixed	No	0	Yes	0	0	0
283	Elias Piña	Comendador	WO71°61'986'	N 19°05, 246'	395	2	sucker	Dom Rep	3	1500	No	None	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
284	Elias Piña	Comendador	WO71°61'986'	N 19°05, 246'	395	2	sucker	Dom Rep	3	1500	No	None	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
285	Elias Piña	Comendador	WO71°61'986'	N 19°05, 246'	395	2	sucker	Dom Rep	3	1500	No	None	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
286	Elias Piña	Comendador	WO71°61'986'	N 19°05, 246'	395	2	sucker	Dom Rep	3	1500	No	None	No	Herbicide	Yes	Mixed	No	0	Yes	0	1	0
287	Elias Piña	Comendador	WO71°61'986'	N 19°05, 246'	395	2	sucker	Dom Rep	3	1500	No	None	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
288	Elias Piña	Comendador	WO71°61'986'	N 19°05, 246'	395	2	sucker	Dom Rep	3	1500	No	None	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
289	Elias Piña	Comendador	WO71°61'986'	N 19°05, 246'	395	2	sucker	Dom Rep	3	1500	No	None	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
290	Elias Piña	Comendador	WO71°61'986'	N 19°05, 246'	395	2	sucker	Dom Rep	3	1500	No	None	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0
291	Elias Piña	Comendador	WO71°61'986'	N 19°05, 246'	395	2	sucker	Dom Rep	3	1500	No	None	No	Herbicide	Yes	Mixed	No	0	Yes	0	0	0

Positive results are highlighted in yellow

Annexes

Annex 2: Full indexing results for the MxH samples collected during the nationwide survey

Sample	Sampling location		GPS coordinates			Plot superficy (ha)	Planting material	Origin of plants	Age of plot (year)	Plant density (pl/ha)	Irrigation	type d'irrigation	Crop association	Weed control	Banana surrounding	Sigatoka control	BSV symptoms on plot	Sigatoka severity index	Mealybugs on the plot	indexations		
	Province	Municipality	Longitude (west)	Latitude (north)	Altitude (m)															BSOLV	BSGFV	BSIMV
1	Monte Cristi	Jaramillo	WO 71° 34,159'	N 19° 45,662'	22	2	vitroplant	Dom Rep	3	3000	Yes	Inundation	No	Manual	Yes	None	No	7,605	Yes	0	0	0
2	Monte Cristi	Jaramillo	WO 71° 34,159'	N 19° 45,662'	22	2	vitroplant	Dom Rep	3	3000	Yes	Inundation	No	Manual	Yes	None	No	7,605	Yes	0	0	0
3	Monte Cristi	Jaramillo	WO 71° 34,159'	N 19° 45,662'	22	2	vitroplant	Dom Rep	3	3000	Yes	Inundation	No	Manual	Yes	None	No	7,605	Yes	0	0	0
4	Monte Cristi	Jaramillo	WO 71° 34,159'	N 19° 45,662'	22	2	vitroplant	Dom Rep	3	3000	Yes	Inundation	No	Manual	Yes	None	No	7,605	Yes	0	0	0
5	Monte Cristi	Jaramillo	WO 71° 34,159'	N 19° 45,662'	22	2	vitroplant	Dom Rep	3	3000	Yes	Inundation	No	Manual	Yes	None	No	7,605	Yes	0	0	0
6	Monte Cristi	Jaramillo	WO 71° 34,159'	N 19° 45,662'	22	2	vitroplant	Dom Rep	3	3000	Yes	Inundation	No	Manual	Yes	None	No	7,605	Yes	0	0	0
7	Monte Cristi	Jaramillo	WO 71° 34,159'	N 19° 45,662'	22	2	vitroplant	Dom Rep	3	3000	Yes	Inundation	No	Manual	Yes	None	No	7,605	Yes	0	0	0
8	Monte Cristi	Jaramillo	WO 71° 34,159'	N 19° 45,662'	22	2	vitroplant	Dom Rep	3	3000	Yes	Inundation	No	Manual	Yes	None	No	7,605	Yes	0	0	0
9	Monte Cristi	Palo Verde	WO 71° 34,497'	N 19° 44,436'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	No	Manual	Yes	Deleafing	No	2,63	Yes	0	0	0
10	Monte Cristi	Palo Verde	WO 71° 34,498'	N 19° 44,436'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	No	Manual	Yes	Deleafing	No	2,63	Yes	0	0	0
11	Monte Cristi	Palo Verde	WO 71° 34,499'	N 19° 44,436'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	No	Manual	Yes	Deleafing	No	2,63	Yes	0	0	0
12	Monte Cristi	Palo Verde	WO 71° 34,500'	N 19° 44,436'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	No	Manual	Yes	Deleafing	No	2,63	Yes	0	0	0
13	Monte Cristi	Palo Verde	WO 71° 34,501'	N 19° 44,436'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	No	Manual	Yes	Deleafing	No	2,63	Yes	0	0	0
14	Monte Cristi	Palo Verde	WO 71° 34,502'	N 19° 44,436'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	No	Manual	Yes	Deleafing	No	2,63	Yes	0	0	0
15	Monte Cristi	Palo Verde	WO 71° 34,503'	N 19° 44,436'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	No	Manual	Yes	Deleafing	No	2,63	Yes	0	0	0
16	Monte Cristi	Palo Verde	WO 71° 34,504'	N 19° 44,436'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	No	Manual	Yes	Deleafing	No	2,63	Yes	0	0	0
17	Monte Cristi	Palo Verde	WO 71° 34,505'	N 19° 44,436'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	No	Manual	Yes	Deleafing	No	2,63	Yes	0	0	0
18	Puerto Plata	La Rotonda	WO 71° 03,616'	N 19° 49,867'	19	4,4	Sucker	Other	1	4800	Yes	Inundation	No	Mixed	No	Mixed	No	21,617	No	0	1	0
19	Puerto Plata	La Rotonda	WO 71° 03,616'	N 19° 49,867'	19	4,4	Sucker	Other	1	4800	Yes	Inundation	No	Mixed	No	Mixed	No	21,617	No	0	0	0
20	Puerto Plata	La Rotonda	WO 71° 03,616'	N 19° 49,867'	19	4,4	Sucker	Other	1	4800	Yes	Inundation	No	Mixed	No	Mixed	No	21,617	No	0	0	0
21	Puerto Plata	La Rotonda	WO 71° 03,616'	N 19° 49,867'	19	4,4	Sucker	Other	1	4800	Yes	Inundation	No	Mixed	No	Mixed	No	21,617	No	0	1	0
22	Puerto Plata	La Rotonda	WO 71° 03,616'	N 19° 49,867'	19	4,4	Sucker	Other	1	4800	Yes	Inundation	No	Mixed	No	Mixed	No	21,617	No	0	1	0
23	Puerto Plata	La Rotonda	WO 71° 03,616'	N 19° 49,867'	19	4,4	Sucker	Other	1	4800	Yes	Inundation	No	Mixed	No	Mixed	No	21,617	No	0	0	0
24	Puerto Plata	La Rotonda	WO 71° 03,616'	N 19° 49,867'	19	4,4	Sucker	Other	1	4800	Yes	Inundation	No	Mixed	No	Mixed	No	21,617	No	0	0	0
25	Puerto Plata	La Rotonda	WO 71° 03,616'	N 19° 49,867'	19	4,4	Sucker	Other	1	4800	Yes	Inundation	No	Mixed	No	Mixed	No	21,617	No	0	0	0
26	Puerto Plata	La Rotonda	WO 71° 03,616'	N 19° 49,867'	19	4,4	Sucker	Other	1	4800	Yes	Inundation	No	Mixed	No	Mixed	No	21,617	No	0	0	0
27	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	0	0
28	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	0	0
29	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	1	0
30	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	0	0
31	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	1	0
32	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	0	0
33	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	0	0
34	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	1	0
35	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	0	0
36	Puerto-Plata	La Balsa	WO 71° 02,813'	N 19° 49,493'	24	0,6	Sucker	Dom Rep	1	3178	Yes	Inundation	No	Manual	Yes	Deleafing	Yes	16,069	Yes	0	0	0
37	Valverde Mao	Sabana Grande	WO 71° 04,245'	19° 31,687'	83	8	Sucker	Dom Rep	1	3000	Yes	Inundation	No	Herbicide	Yes	Mixed	No	2,898	No	0	0	0
38	Valverde Mao	Sabana Grande	WO 71° 04,245'	19° 31,687'	83	8	Sucker	Dom Rep	1	3000	Yes	Inundation	No	Herbicide	Yes	Mixed	No	2,898	No	0	0	0
39	Valverde Mao	Sabana Grande	WO 71° 04,245'	19° 31,687'	83	8	Sucker	Dom Rep	1	3000	Yes	Inundation	No	Herbicide	Yes	Mixed	No	2,898	No	0	0	0

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Contribution to the assessment of the risk of spreading banana streak viruses (BSVs) in the Dominican Republic through the cultivation of banana interspecific hybrids harbouring infectious endogenous BSV sequences.

Annexes

40	Valverde Mao	Sabana Grande	WO 71° 04,245'	19° 31,687'	83	8	Sucker	Dom Rep	1	3000	Yes	Inundation	No	Herbicide	Yes	Mixed	No	2,898	No	0	0	0
41	Valverde Mao	Sabana Grande	WO 71° 04,245'	19° 31,687'	83	8	Sucker	Dom Rep	1	3000	Yes	Inundation	No	Herbicide	Yes	Mixed	No	2,898	No	0	0	0
42	Valverde Mao	Sabana Grande	WO 71° 04,245'	19° 31,687'	83	8	Sucker	Dom Rep	1	3000	Yes	Inundation	No	Herbicide	Yes	Mixed	No	2,898	No	0	0	0
43	Valverde Mao	Sabana Grande	WO 71° 04,245'	19° 31,687'	83	8	Sucker	Dom Rep	1	3000	Yes	Inundation	No	Herbicide	Yes	Mixed	No	2,898	No	0	0	0
44	Valverde Mao	Sabana Grande	WO 71° 04,245'	19° 31,687'	83	8	Sucker	Dom Rep	1	3000	Yes	Inundation	No	Herbicide	Yes	Mixed	No	2,898	No	0	0	0
45	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
46	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
47	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
48	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
49	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
50	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
51	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
52	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
53	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
54	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
55	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
56	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
57	Valverde	Boca de Mao	WO 71° 02,636'	N 19° 35,845'	72	2,2	Sucker	Other	1,3	3178	Yes	Inundation	No	Mixed	Yes	Mixed	Yes	3,622	Yes	0	0	0
58	Valverde Mao	Esperanza	WO 71° 01,670'	N 19° 35,016'	74	1,9	Sucker	Dom Rep	1	4450	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,945	No	0	0	0
59	Valverde Mao	Esperanza	WO 71° 01,670'	N 19° 35,016'	74	1,9	Sucker	Dom Rep	1	4450	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,945	No	0	0	0
60	Valverde Mao	Esperanza	WO 71° 01,670'	N 19° 35,016'	74	1,9	Sucker	Dom Rep	1	4450	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,945	No	0	0	0
61	Valverde Mao	Esperanza	WO 71° 01,670'	N 19° 35,016'	74	1,9	Sucker	Dom Rep	1	4450	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,945	No	0	0	0
62	Valverde Mao	Esperanza	WO 71° 01,670'	N 19° 35,016'	74	1,9	Sucker	Dom Rep	1	4450	Yes	Inundation	No	Manual	Yes	Mixed	Yes	0,945	No	1	0	0

Annexes

92	Santiago	Banegas	WO 70° 47,099	N 19° 30,957	150	3,1	Sucker	Dom Rep	3	2900	Yes	Inundation	No	Mixed	Yes	Mixed	No	8,565	Yes	0	0	0
93	Santiago	Banegas	WO 70° 47,099	N 19° 30,957	150	3,1	Sucker	Dom Rep	3	2900	Yes	Inundation	No	Mixed	Yes	Mixed	No	8,565	Yes	0	1	0
94	Santiago	Banegas	WO 70° 47,099	N 19° 30,957	150	3,1	Sucker	Dom Rep	3	2900	Yes	Inundation	No	Mixed	Yes	Mixed	No	8,565	Yes	0	0	0
95	Santiago	Banegas	WO 70° 47,099	N 19° 30,957	150	3,1	Sucker	Dom Rep	3	2900	Yes	Inundation	No	Mixed	Yes	Mixed	No	8,565	Yes	0	0	0
96	Santiago	Banegas	WO 70° 47,099	N 19° 30,957	150	3,1	Sucker	Dom Rep	3	2900	Yes	Inundation	No	Mixed	Yes	Mixed	No	8,565	Yes	0	0	0
97	Santiago	Banegas	WO 70° 47,099	N 19° 30,957	150	3,1	Sucker	Dom Rep	3	2900	Yes	Inundation	No	Mixed	Yes	Mixed	No	8,565	Yes	0	0	0
98	Santiago	Banegas	WO 70° 47,099	N 19° 30,957	150	3,1	Sucker	Dom Rep	3	2900	Yes	Inundation	No	Mixed	Yes	Mixed	No	8,565	Yes	0	0	0
99	Santiago	Banegas	WO 70° 47,099	N 19° 30,957	150	3,1	Sucker	Dom Rep	3	2900	Yes	Inundation	No	Mixed	Yes	Mixed	No	8,565	Yes	0	0	0
100	Santiago	Banegas	WO 70° 47,099	N 19° 30,957	150	3,1	Sucker	Dom Rep	3	2900	Yes	Inundation	No	Mixed	Yes	Mixed	No	8,565	Yes	0	0	0
101	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	0	0
102	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	0	0
103	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	0	0
104	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	0	0
105	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	0	0
106	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	0	0
107	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	0	0
108	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	0	0
109	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	0	0
110	Santiago	La Canela	WO 70° 48,663'	N19° 29,459'	156	0,1	Sucker	Dom Rep	0,9	1900	Yes	Inundation	No	Manual	No	Deleafing	Yes	1,621	Yes	0	1	0
111	Santiago	La Canela	WO 70° 48,454'	N 19° 28,496'	183	1,2	Sucker	Dom Rep	3,5	2200	Yes	Inundation	oui	Mixed	Yes	Deleafing	No	4,126	Yes	0	0	0
112	Santiago	La Canela	WO 70° 48,454'	N 19° 28,496'	183	1,2	Sucker	Dom Rep	3,5	2200	Yes	Inundation	oui	Mixed	Yes	Deleafing	No	4,126	Yes	0	0	0
113	Santiago	La Canela	WO 70° 48,454'	N 19° 28,496'	183	1,2	Sucker	Dom Rep	3,5	2200	Yes	Inundation	oui	Mixed	Yes	Deleafing	No	4,126	Yes	0	0	0
114	Santiago	La Canela	WO 70° 48,454'	N 19° 28,496'	183	1,2	Sucker	Dom Rep	3,5	2200	Yes	Inundation	oui	Mixed	Yes	Deleafing	No	4				

Annexes

[illegible]

Annexes

196	Espallat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	8,8	Sucker	Dom Rep	4	1112	No	None	No	Mixed	Yes	Mixed	Yes	11,214	Yes	0	0	0
197	Espallat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	8,8	Sucker	Dom Rep	4	1112	No	None	No	Mixed	Yes	Mixed	Yes	11,214	Yes	0	0	0
198	Espallat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	8,8	Sucker	Dom Rep	4	1112	No	None	No	Mixed	Yes	Mixed	Yes	11,214	Yes	0	0	0
199	Espallat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	8,8	Sucker	Dom Rep	4	1112	No	None	No	Mixed	Yes	Mixed	Yes	11,214	Yes	0	0	0
200	Espallat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	8,8	Sucker	Dom Rep	4	1112	No	None	No	Mixed	Yes	Mixed	Yes	11,214	Yes	0	0	0
201	Espallat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	8,8	Sucker	Dom Rep	4	1112	No	None	No	Mixed	Yes	Mixed	Yes	11,214	Yes	0	0	0
202	Espallat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	8,8	Sucker	Dom Rep	4	1112	No	None	No	Mixed	Yes	Mixed	Yes	11,214	Yes	0	0	0
203	Espallat	Rosa 2	WO 70° 30,187'	N 19° 20,928'	157	8,8	Sucker	Dom Rep	4	1112	No	None	No	Mixed	Yes	Mixed	Yes	11,214	Yes	0	0	0
204	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
205	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
206	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
207	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
208	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
209	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
210	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
211	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
212	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
213	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
214	Espallat	Zafaralla 1	WO 70° 29,184'	N 19° 22,454'	180	3,7	Sucker	Dom Rep	1	1271	No	None	No	Mixed	Yes	None	No	12,738	Yes	0	0	0
215	Espallat	Zafaralla 2	WO 70° 29,197'	N 19° 22,534'	186	1	Sucker	Dom Rep	1	1800	No	None	No	Mixed	Yes	Deleafing	No	19,262	No	0	0	0
216	Espallat	Zafaralla 2	WO 70° 29,197'	N 19° 22,534'	186	1	Sucker	Dom Rep	1	1800	No	None	No	Mixed	Yes	Deleafing	No	19,262	No	0	0	0
217	Espallat	Zafaralla 2	WO 70° 29,197'	N 19° 22,534'	186	1	Sucker	Dom Rep	1	1800	No	None	No	Mixed	Yes	Deleafing	No	19,262	No	0	0	0
218	Espallat	Zafaralla 2	WO 70° 29,197'	N 19° 22,534'	186	1	Sucker	Dom Rep	1	1800	No	None	No	Mixed</								

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248	La Vega	Barranca 2	WO 70° 27,136'	N 19° 15,591'	107	12,58	Sucker	Dom Rep	9	1600	No	None	No	Mixed	Yes	Fungicide	No	22,089	Yes	0	0	0
249	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
250	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
251	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
252	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
253	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
254	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
255	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
256	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
257	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
258	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
259	La Vega	Barranca 3	WO 70° 27,560'	N 19° 15,576'	107	4,6	Sucker	Dom Rep	8,5	2384	No	None	No	Mixed	Yes	Fungicide	No	14,898	Yes	0	0	0
260	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
261	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
262	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
263	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
264	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
265	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
266	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
267	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
268	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
269	Monte Plata	Bayaguana	WO 70° 27,654'	N 19° 15,565'	86	1,4	Sucker	Dom Rep	2	1987	No	None	No	Mixed	Yes	Deleafing	No	19,267	Yes	0	0	0
270	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Fungicide	Yes	0	Yes	0	0	0
271	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Fungicide	Yes	0	Yes	0	0	0
272	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Fungicide	Yes	0	Yes	0	0	0
273	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Fungicide	Yes	0	Yes	0	0	0
274	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Fungicide	Yes	0	Yes	0	1	0
275	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Fungicide	Yes	0	Yes	0	0	0
276	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Fungicide	Yes	0	Yes	1	0	0
277	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Fungicide	Yes	0	Yes	0	0	0
278	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Fungicide	Yes	0	Yes	0	0	0
279	Azua	Azua	WO70° 73, 33, 321'	N18°45, 001'	76	8,5	Sucker	Dom Rep	4	1800	No	None	No	Mixed	Yes	Deleafing	No	0	Yes	0	0	0
280	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
281	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
282	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
283	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
284	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
285	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
286	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
287	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
288	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
289	San Juan	Pedro Corto	WO71°23, 332'	N 18°80, 213'	415	3,2	Sucker	Dom Rep	6	1350	No	None	No	Mixed	Yes	Deleafing	No	0	No	0	0	0
290	Elias Piña	Comendador	WO71° 42' 824	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0
291	Elias Piña	Comendador	WO71° 42' 825	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0
292	Elias Piña	Comendador	WO71° 42' 826	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0
293	Elias Piña	Comendador	WO71° 42' 827	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0
294	Elias Piña	Comendador	WO71° 42' 828	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0
295	Elias Piña	Comendador	WO71° 42' 829	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0
296	Elias Piña	Comendador	WO71° 42' 830	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0
297	Elias Piña	Comendador	WO71° 42' 831	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0
298	Elias Piña	Comendador	WO71° 42' 832	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0
299	Elias Piña	Comendador	WO71° 42' 833	N18° 52' 35'	395	1,2	Sucker	Dom Rep	2	1100	No	None	No	Mixed	Yes	effeuillage	No	0	No	0	0	0

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Contribution to the assessment of the risk of spreading banana streak viruses (BSVs) in the Dominican Republic through the cultivation of banana interspecific hybrids harbouring infectious endogenous BSV sequences.

Annexes

290	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	0	0
291	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	0	0
292	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	0	0
293	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	0	0
294	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	1	0
295	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	0	0
296	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	0	0
297	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	0	0
298	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	0	0
299	Elias Piña	Comendador	WO71'61'986'	N 19°05, 246'	395	2,5	Sucker	Dom Rep	10	1100	No	None	No	Mixed	Yes	Fungicide	No	0	No	0	0	0

Annexes

Annex 3: Full indexing results for the FHIA-21 samples collected during in depth survey

Sample	Sampling location	GPS coordinates			Plot superficy (ha)	Planting material	Origin of plants	Age of plot (year)	Plant density (p/ha)	Irrigation	type d'irrigation	Crop association	Weed control	Banana surrounding	Sigatoka control	BSV symptoms on plot	Sigatoka severity index	Mealybugs on the plot	Daily temparture differences			indexations		
		Longitude (west)	Latitude (north)	Altitude (m)															Average 1 month before sampling	Average 3 month before sampling	Average 6 month before sampling	BSOLV	B5GFV	BSIMV
1	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
2	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	1	6,316	oui	10,2	10,3	10,4	0	1	0
3	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
4	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	1	6,316	oui	10,2	10,3	10,4	0	0	0
5	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
6	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
7	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
8	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
9	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
10	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
11	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
12	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
13	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
14	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
15	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
16	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	1	6,316	oui	10,2	10,3	10,4	0	0	0
17	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
18	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	1	6,316	oui	10,2	10,3	10,4	0	0	0
19	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
20	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
21	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
22	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
23	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
24	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
25	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
26	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
27	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
28	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
29	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
30	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
31	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
32	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	1	0	0
33	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
34	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
35	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
36	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
37	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
38	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	1	6,316	oui	10,2	10,3	10,4	0	1	0
39	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
40	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
41	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
42	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
43	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
44	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	1	0
45	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	1	6,316	oui	10,2	10,3	10,4	0	1	0
46	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0

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Contribution to the assessment of the risk of spreading banana streak viruses (BSVs) in the Dominican Republic through the cultivation of banana interspecific hybrids harbouring infectious endogenous BSV sequences.

Annexes

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Annexes

99	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
100	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
101	Montecristi- Jaramillo	WO 71° 34,159'	N 19° 44,524'	22	0,629	vitroplant	Costa Rica	10	2100	Yes	Inundation	No	Mixed	Yes	Deleafing	0	6,316	oui	10,2	10,3	10,4	0	0	0
102	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	0	0
103	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	1	9,754	oui	9,3	9,2	9,4	0	0	0
104	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	1	0
105	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	0	0
106	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	0	0
107	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	0	0
108	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	1	9,754	oui	9,3	9,2	9,4	0	0	0
109	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	0	0
110	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	1	0
111	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	1	0
112	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	1	0
113	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	1	0
114	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	0	0
115	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	0	0
116	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	0	0
117	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	1	0
118	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No	None	Yes	Mixed	0	9,754	oui	9,3	9,2	9,4	0	0	0
119	Puerto Plata-Belloso	WO 71° 01,018'	N 19° 50,173'	25	12	Sucker	Dom Rep	1	3179	Yes	Inundation	No												

Annexes

[illegible]

Positive results are highlighted in yellow

Annexes

Annex 4: Full indexing results for the MxH samples collected during in depth survey

Sample	Sampling location	GPS coordinates			Plot superficy (ha)	Planting material	Origin of plants	Age of plot (year)	Plant density (pl/ha)	Irrigation	type d'Irrigation	Crop association	Weed control	Banana surrounding	Sigatoka control	BSV symptoms on plot	Sigatoka severity index	Mealybugs on the plot	Daily temperture differences			indexations		
		Longitude (west)	Latitude (north)	Altitude (m)															Average 1 month before sampling	Average 3 month before sampling	Average 6 month before sampling	BSOLV	BSGFV	BSIMV
1	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
2	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
3	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
4	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
5	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
6	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
7	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
8	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
9	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
10	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
11	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
12	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
13	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
14	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
15	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
16	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
17	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	1	10,2	10,5	10,4	0	0	0
18	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	1	10,2	10,5	10,4	0	0	0
19	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
20	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	1	0
21	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
22	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	1	10,2	10,5	10,4	0	0	0
23	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
24	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
25	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	1	2,632	0	10,2	10,5	10,4	0	0	0
26	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
27	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
28	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
29	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
30	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
31	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	1	0
32	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
33	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
34	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	1	10,2	10,5	10,4	0	0	0
35	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
36	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	1	0
37	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
38	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
39	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
40	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
41	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	1	2,632	1	10,2	10,5	10,4	0	0	0
42	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0

PhD thesis R.-T. Martinez – 14 December 2015 – Université des Antilles

Contribution to the assessment of the risk of spreading banana streak viruses (BSVs) in the Dominican Republic through the cultivation of banana interspecific hybrids harbouring infectious endogenous BSV sequences.

Annexes

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Annexes

95	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
96	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
97	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
98	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	1	10,2	10,5	10,4	0	0	0
99	Montecristi-Palo Verde	WO 71° 34,566'	N 19° 44,524'	18	1,5	Sucker	Dom Rep	12	1500	Yes	Inundation	None	Mixed	Yes	Fungicide	0	2,632	0	10,2	10,5	10,4	0	0	0
100	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	10,2	10,5	10,4	0	0	0
101	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	10,2	10,5	10,4	0	0	0
102	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	10,2	10,5	10,4	0	0	0
103	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	9,4	9,2	9,4	0	0	0
104	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	1	6,08	0	9,4	9,2	9,4	0	0	0
105	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	9,4	9,2	9,4	0	0	0
106	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	9,4	9,2	9,4	0	0	0
107	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	9,4	9,2	9,4	0	0	0
108	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	9,4	9,2	9,4	0	0	0
109	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	9,4	9,2	9,4	0	0	0
110	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	9,4	9,2	9,4	0	0	0
111	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	1	9,4	9,2	9,4	0	0	0
112	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	1	9,4	9,2	9,4	0	0	0
113	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	9,4	9,2	9,4	0	0	0
114	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Defolating	0	6,08	0	9,4	9,2	9,4	0	0	0
115	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25																				

Annexes

[illegible]

Annexes

199	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Deleafing	0	6,084	0	9,4	9,2	9,4	0	0	0
200	Puerto Plata-Belloso	WO 71° 02,813'	N 19° 50,173'	25	4	Sucker	Dom Rep	2,5	2100	Yes	Inundation	None	Mixed	Yes	Deleafing	0	6,084	0	9,4	9,2	9,4	0	0	0

Positive results are highlighted in yellow

Annexes

Annex 5: Full indexing results for the Cavendish samples collected in 5 provinces

Sample	Sampling location		GPS coordinates			Planting material	Age of plot (year)	Plant density (pl/ha)	Irrigation	Irrigation type	Black Sigatoka symptoms	BSV symptoms	Indexings		
	Province	Municipality	Longitude (west)	Latitude (north)	Plot superfcy (ha)								BSOLV	BSGFV	BSIMV
1	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
2	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
3	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
4	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
5	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
6	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
7	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
8	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
9	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
10	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
11	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
12	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
13	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
14	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
15	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
16	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
17	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
18	Azua	Finca 1	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
19	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
20	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
21	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
22	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
23	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
24	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
25	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
26	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
27	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
28	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
29	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
30	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
31	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
32	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
33	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
34	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	1	0	0
35	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
36	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
37	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
38	Azua	Finca 2	NA	NA	800	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
39	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
40	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
41	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
42	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
43	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
44	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
45	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
46	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	1	0	0
47	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
48	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0

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Contribution to the assessment of the risk of spreading banana streak viruses (BSVs) in the Dominican Republic through the cultivation of banana interspecific hybrids harbouring infectious endogenous BSV sequences.

Annexes

49	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
50	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
51	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
52	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
53	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
54	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
55	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
56	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
57	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
58	Azua	Finca 3	NA	NA	600	sucker	10	2400	yes	Flooding	Yes	No	0	0	0
59	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
60	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
61	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
62	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
63	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
64	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
65	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
66	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
67	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
68	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
69	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
70	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
71	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
72	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
73	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	1	0	0
74	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
75	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	1	0	0
76	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
77	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
78	Azua	Finca 4	NA	NA	900	sucker	15	2400	yes	Flooding	Yes	No	0	0	0
79	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
80	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
81	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
82	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
83	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
84	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
85	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
86	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
87	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
88	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
89	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
90	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
91	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
92	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
93	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
94	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
95	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
96	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
97	Mao	Pueblo Nuevo	WO 71° 50,2469'	N 19° 38,345'	2000	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
98	Montecristi	Palo Verde	WO 71° 28,428'	N 19° 20,235'	1300	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
99	Montecristi	Palo Verde	WO 71° 28,428'	N 19° 20,235'	1300	sucker	10	2400	yes	Gravity	Yes	No	0	0	0
100	Montecristi	Palo Verde	WO 71° 28,428'	N 19° 20,235'	1300	sucker	10	2400	yes	Gravity	Yes	No	0	0	0

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Contribution to the assessment of the risk of spreading banana streak viruses (BSVs) in the Dominican Republic through the cultivation of banana interspecific hybrids harbouring infectious endogenous BSV sequences.

Annexes

[illegible]

Annexes

[illegible]

Annexes

205	Santiago	Banegas -1	WO 70° 47,787'	N 19° 31,838'	1000	sucker	10	2400	yes	Mixed	Yes	No	0	0	0
206	Santiago	Banegas -1	WO 70° 47,787'	N 19° 31,838'	1000	sucker	10	2400	yes	Mixed	Yes	No	0	0	0
207	Santiago	Banegas -1	WO 70° 47,787'	N 19° 31,838'	1000	sucker	10	2400	yes	Mixed	Yes	No	0	0	0
208	Santiago	Banegas -1	WO 70° 47,787'	N 19° 31,838'	1000	sucker	10	2400	yes	Mixed	Yes	No	0	0	0
209	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	800	sucker	6	2560	yes	Gravity	Yes	No	0	0	0
210	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
211	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
212	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
213	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
214	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
215	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
216	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
217	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
218	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
219	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
220	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
221	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
222	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
223	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
224	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
225	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
226	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
227	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
228	Santiago	Banegas -2	WO 70° 50,604'	N 19° 33,055'	180	sucker	6	2400	yes	Gravity	Yes	No	0	0	0
229	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
230	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
231	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
232	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
233	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
234	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
235	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
236	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
237	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
238	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
239	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
240	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
241	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
242	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
243	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
244	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
245	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
246	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
247	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0
248	Santiago	Banegas -3	WO 71° 12,546'	N 19° 33,250'	1400	sucker	10	2560	yes	Gravity	Yes	No	0	0	0

Positive results are highlighted in yellow

Annexes

Annex 6: eBSOLV patterns of FHIA-21 and MxH samples from the nationwide surveys

Sample	Variety	Genotype	Sampling location		signature eBSOLV								Allelic pattern
			Province	Municipality	16-17	18-19	20-21	23-24	25-26	27-28	29-30	DifOL	
Infectious allele pattern					+	-	-	+	+	+	+	+	OL1
Non-infectious allele pattern					+	+	+	-	+	+	+	+	OL2
1	FHIA-21	AAAB	Montecristi	Jaramillo	+	-	-	+	+	+	+	+	OL1
2	FHIA-21	AAAB	Montecristi	Palo Verde	+	-	-	+	+	+	+	+	OL1
3	FHIA-21	AAAB	Puerto Plata	La Balsa	+	-	-	+	+	+	+	+	OL1
4	FHIA-21	AAAB	Puerto Plata	Belloso	+	-	-	+	+	+	+	+	OL1
5	FHIA-21	AAAB	Valverde Mao	Sabana Grande	+	-	-	+	+	+	+	+	OL1
6	FHIA-21	AAAB	Valverde Mao	Boca de Mao	+	-	-	+	+	+	+	+	OL1
7	FHIA-21	AAAB	Valverde Mao	Esperanza	+	-	-	+	+	+	+	+	OL1
8	FHIA-21	AAAB	Valverde Mao	La Caida	+	-	-	+	+	+	+	+	OL1
9	FHIA-21	AAAB	Santiago-Banegas1	Banegas 1	+	-	-	+	+	+	+	+	OL1
10	FHIA-21	AAAB	Santiago-Banegas 2	Banegas 2	+	-	-	+	+	+	+	+	OL1
11	FHIA-21	AAAB	Santiago-Hatillo	San Lorenzo1	+	-	-	+	+	+	+	+	OL1
12	FHIA-21	AAAB	Hermanas Mirabal	Jayabo	+	-	-	+	+	+	+	+	OL1
13	FHIA-21	AAAB	Hermanas Mirabal	Ceiba 1	+	-	-	+	+	+	+	+	OL1
14	FHIA-21	AAAB	Hermanas Mirabal	Ceiba 2	+	-	-	+	+	+	+	+	OL1
15	FHIA-21	AAAB	Hermanas Mirabal	Ceiba 3	+	-	-	+	+	+	+	+	OL1
16	FHIA-21	AAAB	Hermanas Mirabal	Jayabo 2	+	-	-	+	+	+	+	+	OL1
17	FHIA-21	AAAB	Espaillat	Rosa 2	+	-	-	+	+	+	+	+	OL1
18	FHIA-21	AAAB	La Vega	Jamo	+	-	-	+	+	+	+	+	OL1
19	FHIA-21	AAAB	La Vega	Barranca 2	+	-	-	+	+	+	+	+	OL1
20	FHIA-21	AAAB	La Vega	Barranca 3	+	-	-	+	+	+	+	+	OL1
21	FHIA-21	AAAB	La Vega	Barranca 4	+	-	-	+	+	+	+	+	OL1
22	FHIA-21	AAAB	Azua	Azua	+	-	-	+	+	+	+	+	OL1
23	FHIA-21	AAAB	San Juan	Pajonal	+	-	-	+	+	+	+	+	OL1
24	FHIA-21	AAAB	Elias Piña	Comendador	+	-	-	+	+	+	+	+	OL1
25	MxH	AAB	Monte Cristi	Jaramillo	+	-	-	+	+	+	+	+	OL1
26	MxH	AAB	Monte Cristi	Palo Verde	+	-	-	+	+	+	+	+	OL1
27	MxH	AAB	Puerto Plata	La Rotonda	+	-	-	+	+	+	+	+	OL1
28	MxH	AAB	Puerto-Plata	La Balsa	+	-	-	+	+	+	+	+	OL1
29	MxH	AAB	Valverde Mao	Sabana Grande	+	-	-	+	+	+	+	+	OL1
30	MxH	AAB	Valverde	Boca de Mao	+	-	-	+	+	+	+	+	OL1
31	MxH	AAB	Valverde Mao	Esperanza	+	-	-	+	+	+	+	+	OL1
32	MxH	AAB	Valverde Mao	La Caida	+	-	-	+	+	+	+	+	OL1
33	MxH	AAB	Santiago	Banegas	+	-	-	+	+	+	+	+	OL1
34	MxH	AAB	Santiago	La Canela	+	-	-	+	+	+	+	+	OL1
35	MxH	AAB	Hermanas Mirabal	Jayabo	+	-	-	+	+	+	+	+	OL1
36	MxH	AAB	Hermanas Mirabal	La Ceiba-1	+	-	-	+	+	+	+	+	OL1
37	MxH	AAB	Hermanas Mirabal	La Ceiba-2	+	-	-	+	+	+	+	+	OL1
38	MxH	AAB	Espaillat	Aguacate	+	-	-	+	+	+	+	+	OL1
39	MxH	AAB	Espaillat	Rosa 1	+	-	-	+	+	+	+	+	OL1
40	MxH	AAB	Espaillat	Rosa 2	+	-	-	+	+	+	+	+	OL1
41	MxH	AAB	Espaillat	Zafaralla 1	+	-	-	+	+	+	+	+	OL1
42	MxH	AAB	Espaillat	Zafaralla 2	+	-	-	+	+	+	+	+	OL1
43	MxH	AAB	La Vega	Barranca 1	+	-	-	+	+	+	+	+	OL1
44	MxH	AAB	La Vega	Barranca 2	+	-	-	+	+	+	+	+	OL1
45	MxH	AAB	La Vega	Barranca 3	+	-	-	+	+	+	+	+	OL1
46	MxH	AAB	Monte Plata	Bayaguana	+	-	-	+	+	+	+	+	OL1
47	MxH	AAB	Azua	Azua	+	-	-	+	+	+	+	+	OL1
48	MxH	AAB	San Juan	Pedro Corto	+	-	-	+	+	+	+	+	OL1
49	MxH	AAB	Elias Piña	Comendador	+	-	-	+	+	+	+	+	OL1

Annexes

Annex 7: eBSGFV patterns of FHIA-21 and MxH samples from the nationwide surveys

Sampl e	Variety	Genotyp e	Sampling location		signature eBSGFV												RFLP			Allelic patter n	
			Province	Municipality	VM 1	VM 2	VM2 '	VV 1	VV 2	VV2 '	VV 3	VV 4	VV4 '	VV 5	VV5 '	VV 6	VV6 '	DifG f	442p b		366p b
Infectious allele pattern					+	+	+	+	+	+	+	+	+	-	-	+	+	+	-	+	GF7
Non-infectious allele pattern					+	+	+	+	+	+	+	+	+	-	-	+	+	+	+	-	GF9
1	FHIA-21	AAAB	Montecristi	Jaramillo	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
2	FHIA-21	AAAB	Montecristi	Palo Verde	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
3	FHIA-21	AAAB	Puerto Plata	La Balsa	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
4	FHIA-21	AAAB	Puerto Plata	Belloso	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
5	FHIA-21	AAAB	Valverde Mao	Sabana Grande	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
6	FHIA-21	AAAB	Valverde Mao	Boca de Mao	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
7	FHIA-21	AAAB	Valverde Mao	Esperanza	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
8	FHIA-21	AAAB	Valverde Mao	La Caida	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
9	FHIA-21	AAAB	Santiago-Banegas1	Banegas 1	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
10	FHIA-21	AAAB	Santiago-Banegas 2	Banegas 2	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
11	FHIA-21	AAAB	Santiago-Hatillo	San Lorenzo1	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
12	FHIA-21	AAAB	Hermanas Mirabal	Jayabo	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
13	FHIA-21	AAAB	Hermanas Mirabal	Ceiba 1	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
14	FHIA-21	AAAB	Hermanas Mirabal	Ceiba 2	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
15	FHIA-21	AAAB	Hermanas Mirabal	Ceiba 3	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
16	FHIA-21	AAAB	Hermanas Mirabal	Jayabo 2	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
17	FHIA-21	AAAB	Espaillat	Rosa 2	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
18	FHIA-21	AAAB	La Vega	Jamo	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
19	FHIA-21	AAAB	La Vega	Barranca 2	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
20	FHIA-21	AAAB	La Vega	Barranca 3	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
21	FHIA-21	AAAB	La Vega	Barranca 4	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
22	FHIA-21	AAAB	Azua	Azua	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
23	FHIA-21	AAAB	San Juan	Pajonal	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
24	FHIA-21	AAAB	Elias Piña	Comendador	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
25	MxH	AAB	Monte Cristi	Jaramillo	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
26	MxH	AAB	Monte Cristi	Palo Verde	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
27	MxH	AAB	Puerto Plata	La Rotonda	+	+	MxH	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
28	MxH	AAB	Puerto-Plata	La Balsa	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
29	MxH	AAB	Valverde Mao	Sabana Grande	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
30	MxH	AAB	Valverde	Boca de Mao	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
31	MxH	AAB	Valverde Mao	Esperanza	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
32	MxH	AAB	Valverde Mao	La Caida	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
33	MxH	AAB	Santiago	Banegas	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
34	MxH	AAB	Santiago	La Canela	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
35	MxH	AAB	Hermanas Mirabal	Jayabo	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
36	MxH	AAB	Hermanas Mirabal	La Ceiba-1	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
37	MxH	AAB	Hermanas Mirabal	La Ceiba-2	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
38	MxH	AAB	Espaillat	Aguacate	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
39	MxH	AAB	Espaillat	Rosa 1	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
40	MxH	AAB	Espaillat	Rosa 2	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
41	MxH	AAB	Espaillat	Zafaralla 1	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
42	MxH	AAB	Espaillat	Zafaralla 2	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
43	MxH	AAB	La Vega	Barranca 1	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
44	MxH	AAB	La Vega	Barranca 2	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7

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45	MxH	AAB	La Vega	Barranca 3	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
46	MxH	AAB	Monte Plata	Bayaguana	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
47	MxH	AAB	Azua	Azua	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
48	MxH	AAB	San Juan	Pedro Corto	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7
49	MxH	AAB	Elias Piña	Comendador	+	+	+	-	+	+	+	+	+	-	-	+	+	+	-	+	GF7

Annexes

Annex 8: eBSIM patterns of FHIA-21 and MxH samples from the nationwide surveys

Sample	Variety	Genotype	Sampling location		eBSIMV signature										Allelic pattern
			Province	Municipality	M/F2	M/F2'	F1/F3	F1/F3'	F3/F4	F3/F4'	F4/F5	F4/F5'	F5/M	F5/M'	
Infectious allele pattern					+	+	+	+	+	+	+	+	+	+	IM
1	FHIA-21	AAAB	Montecristi	Jaramillo	-	-	-	-	-	-	-	-	-	-	no eBSIMV
2	FHIA-21	AAAB	Montecristi	Palo Verde	-	-	-	-	-	-	-	-	-	-	no eBSIMV
3	FHIA-21	AAAB	Puerto Plata	La Balsa	-	-	-	-	-	-	-	-	-	-	no eBSIMV
4	FHIA-21	AAAB	Puerto Plata	Belloso	-	-	-	-	-	-	-	-	-	-	no eBSIMV
5	FHIA-21	AAAB	Valverde Mao	Sabana Grande	-	-	-	-	-	-	-	-	-	-	no eBSIMV
6	FHIA-21	AAAB	Valverde Mao	Boca de Mao	-	-	-	-	-	-	-	-	-	-	no eBSIMV
7	FHIA-21	AAAB	Valverde Mao	Esperanza	-	-	-	-	-	-	-	-	-	-	no eBSIMV
8	FHIA-21	AAAB	Valverde Mao	La Caida	-	-	-	-	-	-	-	-	-	-	no eBSIMV
9	FHIA-21	AAAB	Santiago-Banegas1	Banegas 1	-	-	-	-	-	-	-	-	-	-	no eBSIMV
10	FHIA-21	AAAB	Santiago-Banegas 2	Banegas 2	-	-	-	-	-	-	-	-	-	-	no eBSIMV
11	FHIA-21	AAAB	Santiago-Hatillo	San Lorenzo1	-	-	-	-	-	-	-	-	-	-	no eBSIMV
12	FHIA-21	AAAB	Hermanas Mirabal	Jayabo	-	-	-	-	-	-	-	-	-	-	no eBSIMV
13	FHIA-21	AAAB	Hermanas Mirabal	Ceiba 1	-	-	-	-	-	-	-	-	-	-	no eBSIMV
14	FHIA-21	AAAB	Hermanas Mirabal	Ceiba 2	-	-	-	-	-	-	-	-	-	-	no eBSIMV
15	FHIA-21	AAAB	Hermanas Mirabal	Ceiba 3	-	-	-	-	-	-	-	-	-	-	no eBSIMV
16	FHIA-21	AAAB	Hermanas Mirabal	Jayabo 2	-	-	-	-	-	-	-	-	-	-	no eBSIMV
17	FHIA-21	AAAB	Españilat	Rosa 2	-	-	-	-	-	-	-	-	-	-	no eBSIMV
18	FHIA-21	AAAB	La Vega	Jamo	-	-	-	-	-	-	-	-	-	-	no eBSIMV
19	FHIA-21	AAAB	La Vega	Barranca 2	-	-	-	-	-	-	-	-	-	-	no eBSIMV
20	FHIA-21	AAAB	La Vega	Barranca 3	-	-	-	-	-	-	-	-	-	-	no eBSIMV
21	FHIA-21	AAAB	La Vega	Barranca 4	-	-	-	-	-	-	-	-	-	-	no eBSIMV
22	FHIA-21	AAAB	Azua	Azua	-	-	-	-	-	-	-	-	-	-	no eBSIMV
23	FHIA-21	AAAB	San Juan	Pajonal	-	-	-	-	-	-	-	-	-	-	no eBSIMV
24	FHIA-21	AAAB	Elias Piña	Comendador	-	-	-	-	-	-	-	-	-	-	no eBSIMV
25	MxH	AAB	Monte Cristi	Jaramillo	-	-	-	-	-	-	-	-	-	-	no eBSIMV
26	MxH	AAB	Monte Cristi	Palo Verde	-	-	-	-	-	-	-	-	-	-	no eBSIMV
27	MxH	AAB	Puerto Plata	La Rotonda	-	-	-	-	-	-	-	-	-	-	no eBSIMV
28	MxH	AAB	Puerto-Plata	La Balsa	-	-	-	-	-	-	-	-	-	-	no eBSIMV
29	MxH	AAB	Valverde Mao	Sabana Grande	-	-	-	-	-	-	-	-	-	-	no eBSIMV
30	MxH	AAB	Valverde	Boca de Mao	-	-	-	-	-	-	-	-	-	-	no eBSIMV
31	MxH	AAB	Valverde Mao	Esperanza	-	-	-	-	-	-	-	-	-	-	no eBSIMV
32	MxH	AAB	Valverde Mao	La Caida	-	-	-	-	-	-	-	-	-	-	no eBSIMV
33	MxH	AAB	Santiago	Banegas	-	-	-	-	-	-	-	-	-	-	no eBSIMV
34	MxH	AAB	Santiago	La Canela	-	-	-	-	-	-	-	-	-	-	no eBSIMV
35	MxH	AAB	Hermanas Mirabal	Jayabo	-	-	-	-	-	-	-	-	-	-	no eBSIMV
36	MxH	AAB	Hermanas Mirabal	La Ceiba-1	-	-	-	-	-	-	-	-	-	-	no eBSIMV
37	MxH	AAB	Hermanas Mirabal	La Ceiba-2	-	-	-	-	-	-	-	-	-	-	no eBSIMV
38	MxH	AAB	Españilat	Aguacate	-	-	-	-	-	-	-	-	-	-	no eBSIMV
39	MxH	AAB	Españilat	Rosa 1	-	-	-	-	-	-	-	-	-	-	no eBSIMV
40	MxH	AAB	Españilat	Rosa 2	-	-	-	-	-	-	-	-	-	-	no eBSIMV
41	MxH	AAB	Españilat	Zafaralla 1	-	-	-	-	-	-	-	-	-	-	no eBSIMV
42	MxH	AAB	Españilat	Zafaralla 2	-	-	-	-	-	-	-	-	-	-	no eBSIMV
43	MxH	AAB	La Vega	Barranca 1	-	-	-	-	-	-	-	-	-	-	no eBSIMV
44	MxH	AAB	La Vega	Barranca 2	-	-	-	-	-	-	-	-	-	-	no eBSIMV
45	MxH	AAB	La Vega	Barranca 3	-	-	-	-	-	-	-	-	-	-	no eBSIMV
46	MxH	AAB	Monte Plata	Bayaguana	-	-	-	-	-	-	-	-	-	-	no eBSIMV
47	MxH	AAB	Azua	Azua	-	-	-	-	-	-	-	-	-	-	no eBSIMV
48	MxH	AAB	San Juan	Pedro Corto	-	-	-	-	-	-	-	-	-	-	no eBSIMV
49	MxH	AAB	Elias Piña	Comendador	-	-	-	-	-	-	-	-	-	-	no eBSIMV

Annexes

Annex 9: Full indexing results for the plants of the experimental plot

				BSOLV						BSGFV						BSIMV						BSOLV or BSGFV						
Plant N°	Trait	Block	Rank	T0 (planting)	T1 (3 mths)	T2 (6 mths)	T3 (9 mths)	T4 (12 mths)	T5 (15 mths)	T0 (planting)	T1 (3 mths)	T2 (6 mths)	T3 (9 mths)	T4 (12 mths)	T5 (15 mths)	T0 (planting)	T1 (3 mths)	T2 (6 mths)	T3 (9 mths)	T4 (12 mths)	T5 (15 mths)	T0 (planting)	T1 (3 mths)	T2 (6 mths)	T3 (9 mths)	T4 (12 mths)	T5 (15 mths)	
1	T3	1	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2	T1	1	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3	T4	1	R3	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	
4	T5	1	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5	T2	1	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6	T1	2	R1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1	1	
7	T5	2	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
8	T4	2	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
9	T3	2	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
10	T2	2	R5	0	x	x	x	x	x	0	x	x	x	x	x	0	x	x	x	x	x	0	x	x	x	x	x	
11	T4	3	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
12	T1	3	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
13	T2	3	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
14	T5	3	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
15	T3	3	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
16	T3	4	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
17	T1	4	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
18	T4	4	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
19	T5	4	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
20	T2	4	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
21	T1	5	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
22	T5	5	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
23	T3	5	R3	0	0	1	1	1	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	1
24	T4	5	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
25	T2	5	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
26	T3	6	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
27	T1	6	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
28	T4	6	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
29	T5	6	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
30	T2	6	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
31	T4	7	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
32	T3	7	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
33	T1	7	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
34	T5	7	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
35	T2	7	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
36	T5	8	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
37	T3	8	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
38	T2	8	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
39	T4	8	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
40	T1	8	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
41	T2	9	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
42	T5	9	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
43	T1	9	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
44	T4	9	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Annexes

[illegible]

Annexes

97	T3	20	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
98	T1	20	R3	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	1
99	T5	20	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
100	T2	20	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
101	T1	21	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
102	T5	21	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
103	T2	21	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
104	T4	21	R4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
105	T3	21	R5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
106	T4	22	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
107	T5	22	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
108	T2	22	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
109	T1	22	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
110	T3	22	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
111	T5	23	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
112	T3	23	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
113	T4	23	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
114	T1	23	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
115	T2	23	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
116	T2	24	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
117	T3	24	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
118	T4	24	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
119	T5	24	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
120	T1	24	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
121	T1	25	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
122	T3	25	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
123	T2	25	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
124	T4	25	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
125	T5	25	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
126	T5	26	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
127	T4	26	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
128	T2	26	R3	0	0	0	0	1	1	0	0	0	1	1	1	0	0	0	0	0	0	0	1	1	1
129	T1	26	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
130	T3	26	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
131	T1	27	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	T2	27	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
133	T4	27	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
134	T5	27	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
135	T3	27	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
136	T5	28	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
137	T1	28	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	T4	28	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
139	T2	28	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
140	T3	28	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
141	T4	29	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
142	T3	29	R2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
143	T1	29	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
144	T2	29	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	T5	29	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
146	T2	30	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	T5	30	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
148	T4	30	R3	0	x	x	x	x	x	0	x	x	x	x	0	x	x	x	x	x	0	x	x	x	x

PhD thesis R.-T. Martinez – 14 December 2015 – Université des Antilles

Contribution to the assessment of the risk of spreading banana streak viruses (BSVs) in the Dominican Republic through the cultivation of banana interspecific hybrids harbouring infectious endogenous BSV sequences.

Annexes

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Annexes

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Annexes

253	T3	51	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
254	T5	51	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
255	T1	51	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
256	T3	52	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
257	T4	52	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
258	T2	52	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
259	T5	52	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
260	T1	52	R5	0	x	x	x	x	x	0	x	x	x	x	x	0	x	x	x	x	x	0	x	x	x	x	x
261	T3	53	R1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	
262	T1	53	R2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	
263	T4	53	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
264	T2	53	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
265	T5	53	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
266	T4	54	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
267	T1	54	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
268	T2	54	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
269	T5	54	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
270	T3	54	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
271	T2	55	R1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	
272	T1	55	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
273	T4	55	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
274	T5	55	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
275	T3	55	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
276	T5	56	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
277	T2	56	R2	0	0	0	0																				

Annexes

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Annexes

357	T2	72	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
358	T5	72	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
359	T4	72	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
360	T3	72	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
361	T5	73	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
362	T3	73	R2	0	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0
363	T1	73	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
364	T4	73	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
365	T2	73	R5	0	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0
366	T1	74	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
367	T5	74	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
368	T4	74	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
369	T2	74	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
370	T3	74	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
371	T1	75	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
372	T2	75	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
373	T3	75	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
374	T5	75	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
375	T4	75	R5	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
376	T2	76	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
377	T1	76	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
378	T5	76	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
379	T4	76	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
380	T3	76	R5	0	x	x	x	x	x	0	x	x	x	x	0	x	x	x	x	x	0	x	x	x
381	T5	77	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
382	T4	77	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
383	T3	77	R3	0	x	x	x	x	x	0	x	x	x	x	0	x	x	x	x	x	0	x	x	x
384	T1	77	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
385	T2	77	R5	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
386	T1	78	R1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
387	T5	78	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
388	T3	78	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
389	T2	78	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
390	T4	78	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
391	T5	79	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
392	T2	79	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
393	T4	79	R3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
394	T3	79	R4	0	x	x	x	x	x	0	x	x	x	x	0	x	x	x	x	x	0	x	x	x
395	T1	79	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
396	T4	80	R1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
397	T1	80	R2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
398	T3	80	R3	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	1	1
399	T5	80	R4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
400	T2	80	R5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Positive results are highlighted in yellow.

Dead plants are highlighted in purple.

Annex 10: Partial results from a logistic regression on BSGFV infection rates registered at 15 months on the experimental plot, using SAS glimmix procedure

Model Information	
Data Set	WORK.DON
Response Variable	BSGFV_15
Response Distribution	Binary
Link Function	Logit
Variance Function	Default
Variance Matrix	Not blocked
Estimation Technique	Residual PL
Degrees of Freedom Method	Containment

Class Level Information		
Class	Levels	Values
Bloc	80	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
Variet	2	FHIA21 MxH
Veg	2	S VP

Number of Observations Read	320
Number of Observations Used	307

Response Profile		
Ordered Value	BSGFV_15	Total Frequency
1	1	35
2	0	272
The GLIMMIX procedure is modeling the probability that BSGFV_15='1'.		

Dimensions	
G-side Cov. Parameters	1
Columns in X	9
Columns in Z	80
Subjects (Blocks in V)	1
Max Obs per Subject	307

Fit Statistics	
-2 Res Log Pseudo-Likelihood	1581.40
Generalized Chi-Square	285.97
Gener. Chi-Square / DF	0.94

Covariance Parameter Estimates		
Cov Parm	Estimate	Standard Error
Bloc	0.1092	0.4117

Annexes

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Variet	1	224	1.98	0.1610
Veg	1	224	2.07	0.1515
Variet*Veg	1	224	0.86	0.3544

F Test for Variet*Veg Least Squares Means Slice				
Slice	Num DF	Den DF	F Value	Pr > F
Variet FHIA21	1	224	3.37	0.0677

F Test for Variet*Veg Least Squares Means Slice				
Slice	Num DF	Den DF	F Value	Pr > F
Variet MxH	1	224	0.11	0.7385

F Test for Variet*Veg Least Squares Means Slice				
Slice	Num DF	Den DF	F Value	Pr > F
Veg S	1	224	0.10	0.7546

F Test for Variet*Veg Least Squares Means Slice				
Slice	Num DF	Den DF	F Value	Pr > F
Veg VP	1	224	3.28	0.0717

Variet	Veg	BSGFV (15m) LS-Mean	Standard Error Mean	Lower Mean	Upper Mean
FHIA21	S	0.0908	0.03286	0.04355	0.1795
FHIA21	VP	0.1971	0.04603	0.12160	0.3034
MxH	S	0.0768	0.03025	0.03465	0.1617
MxH	VP	0.0918	0.03322	0.04405	0.1814

Variet	BSGFV (15m) LS-Mean	Standard Error Mean	Lower Mean	Upper Mean
FHIA21	0.1354	0.02902	0.08763	0.2033
MxH	0.0840	0.02255	0.04895	0.1404

Veg	BSGFV (15m) LS-Mean	Standard Error Mean	Lower Mean	Upper Mean
S	0.0835	0.02243	0.04867	0.1397
VP	0.1361	0.02917	0.08811	0.2044

Annexes

Annex 11: Plants height, pseudostem girth, number of hands, number of fingers, fingers girth, bunch weight and virological status of plants of the experimental plot upon bunch harvest time

Plant N°	Treatment	Block	Rank	Plant		Fruits / bunches					Indexing		
				Plant height (cm)	Pseudotrunk girth (cm)	Number of hands per bunch	Number of fingers per bunch	Fingers length (cm)	Fingers girth (cm)	Bunch weight (kg)	BSOLV	BSGFV	BSIMV
1	T3	1	R1	310	61	7	22	15	10	13	0	0	0
2	T1	1	R2	273	49	6	70	22	12	12	0	0	0
3	T4	1	R3	302	62	7	23	16	11	14	0	0	0
4	T5	1	R4	258	45	6	74	21	12	12	0	0	0
5	T2	1	R5	244	50	6	60	20	10	8	0	0	0
6	T1	2	R1	263	48	6	74	23	14	13	0	0	0
7	T5	2	R2	298	63	7	22	14	10	15	0	0	0
8	T4	2	R3	305	61	6	23	15	10	13	0	0	0
9	T3	2	R4	239	56	7	126	21	11	18	0	0	0
10	T2	2	R5	x	x	x	x	x	x	x	x	x	x
11	T4	3	R1	330	59	8	24	15	11	15	0	0	0
12	T1	3	R2	251	59	7	98	18	10	11	0	0	0
13	T2	3	R3	265	49	6	62	22	13	12	0	0	0
14	T5	3	R4	279	47	6	72	20	12	10	0	0	0
15	T3	3	R5	320	46	6	24	15	11	15	0	0	0
16	T3	4	R1	312	60	7	23	16	10	13	0	0	0
17	T1	4	R2	309	63	7	25	15	11	15	0	0	0
18	T4	4	R3	260	54	8	114	22	12	16	0	0	0
19	T5	4	R4	268	51	7	118	22	11	17	0	0	0
20	T2	4	R5	303	59	6	23	13	8	14	0	0	0
21	T1	5	R1	292	54	6	62	19	13	10	0	0	0
22	T5	5	R2	290	60	6	24	14	8	11	0	0	0
23	T3	5	R3	252	50	6	69	21	14	12	1	1	0
24	T4	5	R4	276	59	8	112	21	11	16	0	0	0
25	T2	5	R5	273	50	6	72	22	13	14	0	0	0
26	T3	6	R1	274	58	8	108	21	11	16	0	0	0
27	T1	6	R2	270	50	6	70	22	13	12	0	0	0
28	T4	6	R3	286	50	7	85	22	13	17	0	0	0
29	T5	6	R4	300	60	5	24	14	8	12	0	0	0
30	T2	6	R5	295	56	7	23	13	6	10	0	0	0
31	T4	7	R1	315	64	8	25	16	11	13	0	0	0
32	T3	7	R2	285	50	7	86	22	13	15	0	0	0
33	T1	7	R3	278	56	7	88	18	12	9	0	0	0
34	T5	7	R4	325	60	6	24	15	10	14	0	0	0
35	T2	7	R5	290	64	6	22	13	10	14	0	0	0
36	T5	8	R1	306	56	5	22	14	8	11	0	0	0
37	T3	8	R2	290	58	6	23	13	10	11	0	0	0
38	T2	8	R3	305	60	4	21	14	7	14	0	0	0
39	T4	8	R4	268	54	6	70	22	12	12	0	0	0
40	T1	8	R5	277	52	6	72	21	12	14	0	0	0
41	T2	9	R1	286	50	8	93	22	12	15	0	0	0
42	T5	9	R2	276	53	8	87	22	13	16	0	0	0
43	T1	9	R3	290	64	6	22	13	10	14	0	0	0
44	T4	9	R4	268	51	6	75	18	12	11	0	0	0
45	T3	9	R5	303	59	6	23	13	8	14	0	0	0
46	T1	10	R1	300	53	8	87	22	12	14	0	0	0
47	T4	10	R2	270	50	8	89	22	12	17	0	0	0
48	T2	10	R3	280	57	7	78	22	12	16	0	0	0
49	T5	10	R4	325	59	6	22	14	8	12	0	0	0
50	T3	10	R5	280	48	6	76	21	12	13	0	0	0
51	T4	11	R1	280	54	6	70	21	12	13	0	1	0
52	T1	11	R2	266	58	7	75	20	11	15	0	0	0
53	T2	11	R3	289	56	6	78	22	13	14	0	0	0
54	T3	11	R4	272	55	7	75	22	11	12	1	0	0
55	T5	11	R5	284	58	6	73	22	14	14	0	0	0
56	T3	12	R1	283	50	6	74	22	13	12	0	0	0
57	T5	12	R2	279	58	7	70	22	12	17	0	0	0
58	T4	12	R3	281	52	6	76	23	14	15	0	0	0
59	T2	12	R4	249	55	7	92	19	12	14	0	0	0

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60	T1	12	R5	288	50	7	80	20	13	13	0	0	0
61	T1	13	R1	270	49	7	82	22	13	14	0	0	0
62	T5	13	R2	x	x	x	x	x	x	x	x	x	x
63	T4	13	R3	252	60	7	116	23	12	19	0	0	0
64	T2	13	R4	305	59	6	23	16	10	13	0	0	0
65	T3	13	R5	280	54	6	79	22	13	15	0	0	0
66	T2	14	R1	313	62	8	23	15	11	15	0	0	0
67	T1	14	R2	320	59	7	24	15	11	12	0	0	0
68	T4	14	R3	249	61	7	100	21	11	11	0	0	0
69	T5	14	R4	254	66	8	122	23	11	18	0	0	0
70	T3	14	R5	305	61	6	23	15	10	13	0	0	0
71	T1	15	R1	315	64	8	25	16	11	13	0	0	0
72	T4	15	R2	320	63	6	25	15	10	15	0	0	0
73	T5	15	R3	324	60	6	76	23	13	14	0	0	0
74	T2	15	R4	244	51	7	104	23	11	16	0	0	0
75	T3	15	R5	246	52	6	94	22	11	12	0	0	0
76	T1	16	R1	315	62	8	24	14	10	14	0	0	0
77	T3	16	R2	320	62	6	24	15	11	15	0	0	0
78	T4	16	R3	312	60	7	23	16	10	13	0	0	0
79	T2	16	R4	290	55	6	76	22	13	14	0	0	0
80	T5	16	R5	293	52	6	74	24	13	15	0	0	0
81	T4	17	R1	293	52	6	74	24	13	15	0	0	0
82	T1	17	R2	295	54	6	70	22	13	14	0	0	0
83	T5	17	R3	270	49	6	76	23	12	12	0	0	0
84	T3	17	R4	283	34	6	74	20	12	11	0	1	0
85	T2	17	R5	286	57	6	22	14	8	12	0	0	0
86	T5	18	R1	266	57	6	132	22	11	19	0	0	0
87	T1	18	R2	278	50	8	92	20	12	13	0	0	0
88	T4	18	R3	280	52	7	79	21	13	12	0	0	0
89	T2	18	R4	276	52	7	78	21	13	13	0	0	0
90	T3	18	R5	305	60	4	21	14	7	14	0	0	0
91	T3	19	R1	269	55	6	86	19	11	8	0	0	0
92	T1	19	R2	x	x	x	x	x	x	x	x	x	x
93	T5	19	R3	289	53	6	75	22	13	14	0	0	0
94	T2	19	R4	290	55	6	77	22	13	15	0	0	0
95	T4	19	R5	283	34	6	75	24	13	16	0	0	0
96	T4	20	R1	245	49	6	102	21	12	12	0	0	0
97	T3	20	R2	277	56	9	128	21	11	19	0	0	0
98	T1	20	R3	306	56	5	22	14	8	11	0	0	0
99	T5	20	R4	300	57	6	23	13	6	12	0	0	0
100	T2	20	R5	305	60	4	21	14	7	14	0	0	0
101	T1	21	R1	223	46	5	84	21	11	8	0	0	0
102	T5	21	R2	269	49	6	62	22	13	12	0	0	0
103	T2	21	R3	281	61	6	86	19	12	12	0	0	0
104	T4	21	R4	300	50	6	70	21	13	16	0	0	0
105	T3	21	R5	290	64	6	22	13	10	14	0	0	0
106	T4	22	R1	306	56	5	22	14	8	11	0	0	0
107	T5	22	R2	303	59	6	23	13	8	14	0	0	0
108	T2	22	R3	316	57	5	21	13	7	10	0	0	0
109	T1	22	R4	295	61	8	130	22	13	18	0	0	0
110	T3	22	R5	296	61	10	124	21	12	18	0	0	0
111	T5	23	R1	313	39	6	80	24	12	13	0	0	0
112	T3	23	R2	295	54	8	21	14	7	10	0	0	0
113	T4	23	R3	280	54	4	22	12	9	11	0	0	0
114	T1	23	R4	300	57	6	23	13	6	12	0	0	0
115	T2	23	R5	290	62	8	126	22	11	18	0	0	0
116	T2	24	R1	298	53	6	72	21	13	18	0	0	0
117	T3	24	R2	295	56	7	23	13	6	10	0	0	0
118	T4	24	R3	297	50	7	82	20	13	17	0	0	0
119	T5	24	R4	320	63	6	25	15	10	15	0	0	0
120	T1	24	R5	300	50	5	66	22	13	14	0	0	0
121	T1	25	R1	325	60	6	24	15	10	14	0	0	0
122	T3	25	R2	290	48	6	72	22	13	13	0	0	0
123	T2	25	R3	306	56	5	22	14	8	11	0	0	0
124	T4	25	R4	266	52	6	76	21	13	11	0	0	0
125	T5	25	R5	310	61	7	22	15	10	13	0	0	0
126	T5	26	R1	310	49	6	72	22	12	13	0	0	0
127	T4	26	R2	314	56	6	74	23	13	13	0	0	0
128	T2	26	R3	264	59	8	118	21	11	19	0	1	0
129	T1	26	R4	320	59	7	24	15	11	12	0	0	0

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130	T3	26	R5	325	59	6	25	15	11	13	0	0	0
131	T1	27	R1	268	59	6	102	22	11	14	0	0	0
132	T2	27	R2	305	61	6	23	15	10	13	0	0	0
133	T4	27	R3	315	64	8	25	16	11	13	0	0	0
134	T5	27	R4	320	63	6	25	15	10	15	0	0	0
135	T3	27	R5	290	50	7	80	22	12	12	0	0	0
136	T5	28	R1	280	54	6	50	21	13	13	0	0	0
137	T1	28	R2	310	60	7	23	14	10	13	0	0	0
138	T4	28	R3	300	52	6	76	23	13	14	0	0	0
139	T2	28	R4	270	58	8	108	21	11	16	0	0	0
140	T3	28	R5	312	60	7	23	16	13	13	0	0	0
141	T4	29	R1	309	63	7	25	15	11	15	0	0	0
142	T3	29	R2	290	50	6	76	21	12	15	0	0	0
143	T1	29	R3	306	56	5	22	14	8	11	0	0	0
144	T2	29	R4	303	59	6	23	13	8	14	0	0	0
145	T5	29	R5	268	58	7	110	21	11	12	0	0	0
146	T2	30	R1	312	56	7	84	24	13	15	0	0	0
147	T5	30	R2	286	57	6	22	14	8	12	0	0	0
148	T4	30	R3	x	x	x	x	x	x	x	x	x	x
149	T3	30	R4	288	52	7	82	23	12	11	0	0	0
150	T1	30	R5	295	51	6	74	22	13	15	0	0	0
151	T1	31	R1	306	52	6	74	21	13	15	0	0	0
152	T4	31	R2	250	52	7	118	22	13	16	0	0	0
153	T3	31	R3	300	60	5	24	14	8	12	0	0	0
154	T5	31	R4	300	67	6	23	13	10	14	0	0	0
155	T2	31	R5	305	28	5	58	23	13	13	0	0	0
156	T5	32	R1	294	44	5	64	21	12	13	0	0	0
157	T4	32	R2	305	45	6	78	22	14	17	0	0	0
158	T2	32	R3	310	48	7	82	22	13	16	0	0	0
159	T1	32	R4	290	64	6	22	13	10	14	0	0	0
160	T3	32	R5	275	56	8	138	22	11	21	0	0	0
161	T3	33	R1	x	x	x	x	x	x	x	x	x	x
162	T1	33	R2	309	56	8	91	22	15	17	0	0	0
163	T5	33	R3	315	58	6	71	24	13	15	0	0	0
164	T4	33	R4	309	56	5	59	23	13	14	0	0	0
165	T2	33	R5	310	48	5	65	21	12	14	0	0	0
166	T5	34	R1	309	63	7	25	15	11	15	0	0	0
167	T3	34	R2	290	64	6	22	13	10	14	0	0	0
168	T4	34	R3	306	56	5	22	14	8	11	0	0	0
169	T1	34	R4	303	48	7	81	22	13	15	0	1	0
170	T2	34	R5	272	50	6	74	24	13	14	0	0	0
171	T4	35	R1	296	50	6	78	23	13	14	0	0	0
172	T2	35	R2	x	x	x	x	x	x	x	x	x	x
173	T5	35	R3	292	52	8	88	23	12	13	0	0	0
174	T1	35	R4	295	54	8	21	14	7	10	0	0	0
175	T3	35	R5	280	54	4	22	12	9	11	0	0	0
176	T1	36	R1	300	57	6	23	13	6	12	0	0	0
177	T3	36	R2	290	54	6	40	15	14	11	0	0	0
178	T5	36	R3	295	50	6	74	20	12	15	0	0	0
179	T2	36	R4	309	59	8	86	23	14	16	0	0	0
180	T4	36	R5	263	57	7	110	22	11	14	0	0	0
181	T3	37	R1	320	63	6	25	15	10	15	0	0	0
182	T4	37	R2	x	x	x	x	x	x	x	x	x	x
183	T5	37	R3	307	50	6	76	22	13	13	0	0	0
184	T1	37	R4	290	64	6	22	13	10	14	0	0	0
185	T2	37	R5	306	56	5	22	14	8	11	0	0	0
186	T3	38	R1	269	58	8	128	21	12	20	0	0	0
187	T1	38	R2	260	55	8	106	22	12	15	0	0	0
188	T4	38	R3	307	53	7	79	23	13	15	0	0	0
189	T5	38	R4	315	54	8	93	25	14	19	0	0	0
190	T2	38	R5	284	57	8	110	23	11	17	0	0	0
191	T2	39	R1	252	57	8	104	23	11	16	0	0	0
192	T4	39	R2	325	59	6	25	15	11	13	0	0	0
193	T5	39	R3	322	53	8	89	21	12	12	0	0	0
194	T1	39	R4	305	61	6	23	15	10	13	0	0	0
195	T3	39	R5	315	64	8	25	16	11	13	0	0	0
196	T2	40	R1	320	63	6	25	15	10	15	0	0	0
197	T4	40	R2	258	54	8	108	19	11	17	0	0	0
198	T3	40	R3	191	39	8	112	19	12	18	0	0	0
199	T1	40	R4	244	48	7	106	20	11	16	0	0	0

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200	T5	40	R5	290	54	8	92	22	13	18	0	0	0
201	T2	41	R1	258	50	8	114	19	10	18	0	0	0
202	T4	41	R2	312	60	7	23	16	10	13	0	0	0
203	T1	41	R3	309	63	7	25	15	11	15	0	1	0
204	T5	41	R4	323	58	5	68	23	13	12	0	0	0
205	T3	41	R5	306	56	5	22	14	8	11	0	0	0
206	T1	42	R1	x	x	x	x	x	x	x	x	x	x
207	T4	42	R2	305	48	8	84	21	13	15	0	0	0
208	T2	42	R3	290	60	6	24	14	8	11	0	0	0
209	T5	42	R4	319	50	7	79	21	13	14	0	0	0
210	T3	42	R5	325	59	6	22	14	8	12	0	0	0
211	T1	43	R1	310	50	8	81	22	12	16	0	0	0
212	T5	43	R2	280	54	4	22	12	9	11	0	0	0
213	T2	43	R3	300	57	6	23	13	6	12	0	0	0
214	T4	43	R4	282	61	9	134	22	12	21	0	0	0
215	T3	43	R5	300	60	5	24	14	8	12	0	0	0
216	T1	44	R1	280	53	5	62	23	13	16	0	0	0
217	T2	44	R2	322	59	8	83	23	13	17	0	0	0
218	T5	44	R3	258	49	5	67	22	12	12	0	0	0
219	T4	44	R4	330	59	8	24	15	11	15	0	0	0
220	T3	44	R5	325	60	6	24	15	10	14	0	0	0
221	T3	45	R1	297	50	5	68	23	13	13	0	0	0
222	T5	45	R2	306	53	5	66	22	13	12	0	0	0
223	T1	45	R3	300	57	6	23	13	6	12	0	0	0
224	T4	45	R4	290	50	6	70	24	13	13	0	0	0
225	T2	45	R5	298	54	8	90	24	13	16	0	0	0
226	T1	46	R1	320	59	7	24	15	11	12	0	0	0
227	T2	46	R2	317	36	7	80	25	14	18	0	0	0
228	T5	46	R3	309	63	7	25	15	11	15	0	0	0
229	T4	46	R4	290	64	6	22	13	10	14	0	0	0
230	T3	46	R5	323	50	5	70	22	13	12	0	0	0
231	T5	47	R1	241	56	7	104	21	12	16	0	0	0
232	T2	47	R2	263	53	6	62	19	12	6	0	0	0
233	T3	47	R3	250	33	7	88	19	11	11	0	0	0
234	T1	47	R4	298	54	5	67	22	13	13	0	0	0
235	T4	47	R5	326	52	6	79	22	13	17	0	1	0
236	T3	48	R1	316	50	5	71	24	13	14	0	0	0
237	T5	48	R2	280	54	4	22	12	9	11	0	0	0
238	T4	48	R3	300	57	6	23	13	6	12	0	0	0
239	T2	48	R4	305	60	4	21	14	7	14	0	0	0
240	T1	48	R5	306	53	7	90	25	14	19	0	0	0
241	T2	49	R1	295	56	7	23	13	6	10	0	1	0
242	T5	49	R2	293	52	5	74	24	13	15	0	0	0
243	T1	49	R3	228	54	7	86	22	11	12	0	0	0
244	T3	49	R4	270	49	5	76	23	12	12	0	0	0
245	T4	49	R5	227	50	8	112	20	10	17	0	0	0
246	T5	50	R1	290	64	6	22	13	10	14	0	0	0
247	T1	50	R2	306	56	5	22	14	8	11	0	0	0
248	T2	50	R3	278	50	7	92	20	12	13	0	0	0
249	T3	50	R4	310	61	7	22	15	10	13	0	0	0
250	T4	50	R5	236	56	6	84	22	10	13	0	0	0
251	T4	51	R1	312	54	5	73	22	13	13	0	0	0
252	T2	51	R2	320	59	7	24	15	13	12	0	0	0
253	T3	51	R3	322	59	6	83	23	11	17	0	0	0
254	T5	51	R4	258	49	5	67	22	11	12	0	0	0
255	T1	51	R5	305	61	6	23	15	13	13	0	0	0
256	T3	52	R1	315	64	8	25	16	10	13	0	0	0
257	T4	52	R2	320	63	6	25	15	11	15	0	0	0
258	T2	52	R3	330	59	8	24	15	12	15	0	0	0
259	T5	52	R4	250	51	8	76	20	11	10	0	0	0
260	T1	52	R5	x	x	x	x	x	x	x	x	x	x
261	T3	53	R1	300	50	7	85	20	13	11	0	0	0
262	T1	53	R2	326	52	7	92	26	11	19	0	0	0
263	T4	53	R3	263	53	8	81	22	13	10	0	0	0
264	T2	53	R4	280	55	7	57	20	10	12	0	0	0
265	T5	53	R5	290	64	6	22	13	13	14	0	0	0
266	T4	54	R1	323	50	5	70	22	10	12	0	0	0
267	T1	54	R2	280	55	8	105	21	8	18	0	0	0
268	T2	54	R3	316	57	5	21	13	11	10	0	0	0
269	T5	54	R4	258	53	10	142	23	11	25	0	0	0

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270	T3	54	R5	298	54	5	67	22	12	13	0	0	0
271	T2	55	R1	216	42	8	107	20	8	17	0	0	0
272	T1	55	R2	295	54	8	21	14	12	10	0	0	0
273	T4	55	R3	280	54	4	22	12	13	11	0	0	0
274	T5	55	R4	309	50	7	93	26	9	20	0	0	0
275	T3	55	R5	305	60	4	21	14	6	14	0	0	0
276	T5	56	R1	270	50	6	81	22	7	14	0	0	0
277	T2	56	R2	278	50	6	82	22	8	15	0	0	0
278	T3	56	R3	223	54	5	78	21	12	10	0	0	0
279	T4	56	R4	325	59	6	25	15	12	13	0	0	0
280	T1	56	R5	290	55	5	77	22	10	15	0	0	0
281	T2	57	R1	305	61	6	23	15	11	13	0	0	0
282	T5	57	R2	315	64	8	25	16	12	13	0	0	0
283	T1	57	R3	289	53	6	77	23	13	13	0	0	0
284	T3	57	R4	330	59	8	24	15	15	15	0	0	0
285	T4	57	R5	x	x	x	x	x	x	x	x	x	x
286	T2	58	R1	305	54	5	66	22	12	13	0	0	0
287	T4	58	R2	266	54	7	82	23	11	13	0	0	0
288	T3	58	R3	283	48	7	84	25	13	17	0	0	0
289	T5	58	R4	312	60	7	23	16	13	13	0	0	0
290	T1	58	R5	300	50	5	70	21	12	16	0	0	0
291	T1	59	R1	290	64	6	22	13	10	14	0	0	0
292	T3	59	R2	306	56	5	22	14	12	11	0	0	0
293	T5	59	R3	272	58	7	96	23	8	15	0	0	0
294	T4	59	R4	278	59	6	80	21	12	10	0	0	0
295	T2	59	R5	325	49	5	71	24	13	11	0	0	0
296	T2	60	R1	286	57	6	22	14	12	12	0	0	0
297	T1	60	R2	313	39	6	80	24	8	13	0	0	0
298	T3	60	R3	312	58	5	72	22	13	15	0	0	0
299	T4	60	R4	280	54	4	22	12	13	11	0	1	0
300	T5	60	R5	300	57	6	23	13	11	12	0	0	0
301	T3	61	R1	305	60	4	21	14	12	14	0	0	0
302	T2	61	R2	300	60	5	24	14	11	12	0	0	0
303	T5	61	R3	294	51	5	66	22	12	15	0	0	0
304	T4	61	R4	300	48	6	55	20	12	12	0	1	0
305	T1	61	R5	320	63	6	25	15	11	15	0	0	0
306	T3	62	R1	330	59	8	24	15	13	15	0	0	0
307	T4	62	R2	320	60	5	73	24	10	13	0	0	0
308	T2	62	R3	290	48	5	72	22	10	13	0	0	0
309	T1	62	R4	293	50	6	78	23	12	15	0	0	0
310	T5	62	R5	x	x	x	x	x	x	x	x	x	x
311	T3	63	R1	300	53	7	92	23	10	15	0	1	0
312	T5	63	R2	313	62	8	23	15	13	15	0	0	0
313	T2	63	R3	314	56	5	74	23	11	13	0	0	0
314	T4	63	R4	300	52	5	67	23	11	14	0	0	0
315	T1	63	R5	250	54	6	82	23	11	12	0	0	0
316	T2	64	R1	290	64	6	22	13	12	14	0	0	0
317	T3	64	R2	292	50	6	74	21	11	14	0	0	0
318	T4	64	R3	303	59	6	23	13	10	14	0	0	0
319	T5	64	R4	295	48	7	86	23	11	16	0	0	0
320	T1	64	R5	300	49	6	72	22	10	12	0	0	0
321	T4	65	R1	290	50	6	78	22	11	12	0	1	0
322	T1	65	R2	325	59	6	22	14	13	12	0	0	0
323	T5	65	R3	x	x	x	x	x	x	x	x	x	x
324	T3	65	R4	300	52	5	76	23	13	14	0	0	0
325	T2	65	R5	258	58	6	80	21	13	11	0	0	0
326	T5	66	R1	280	64	11	134	21	10	26	0	0	0
327	T3	66	R2	263	55	8	122	22	14	20	0	0	0
328	T4	66	R3	290	50	6	76	21	11	17	0	0	0
329	T1	66	R4	x	x	x	x	x	x	x	x	x	x
330	T2	66	R5	275	61	8	120	22	13	19	0	0	0
331	T2	67	R1	300	52	5	74	22	13	13	0	0	0
332	T5	67	R2	325	60	6	24	15	13	14	0	0	0
333	T4	67	R3	290	64	6	22	13	10	14	0	0	0
334	T3	67	R4	272	55	6	90	22	8	13	0	0	0
335	T1	67	R5	290	63	8	116	21	7	16	0	0	0
336	T5	68	R1	310	61	7	22	15	11	13	0	0	0
337	T3	68	R2	306	52	5	74	21	6	15	0	0	0
338	T1	68	R3	302	62	7	23	16	12	14	0	0	0
339	T4	68	R4	313	62	8	23	15	11	15	0	0	0

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340	T2	68	R5	320	59	7	24	15	14	12	0	0	0
341	T2	69	R1	268	56	8	128	20	13	19	0	0	0
342	T5	69	R2	280	58	6	91	20	10	11	0	0	0
343	T1	69	R3	305	61	6	23	15	14	13	0	0	0
344	T3	69	R4	315	64	8	25	16	13	13	0	0	0
345	T4	69	R5	320	63	6	25	15	12	15	0	0	0
346	T2	70	R1	280	60	8	135	20	8	21	0	0	0
347	T5	70	R2	286	50	6	80	23	11	12	0	0	0
348	T1	70	R3	290	55	6	72	23	12	14	0	0	0
349	T4	70	R4	315	58	5	71	24	11	15	0	0	0
350	T3	70	R5	309	56	5	59	23	11	14	0	0	0
351	T2	71	R1	312	60	7	23	16	13	13	0	0	0
352	T1	71	R2	288	52	6	79	22	12	18	0	0	0
353	T3	71	R3	290	62	6	109	21	10	14	0	0	0
354	T4	71	R4	306	52	5	75	22	12	17	0	0	0
355	T5	71	R5	303	48	6	81	22	8	15	0	0	0
356	T1	72	R1	272	50	6	74	24	11	14	0	0	0
357	T2	72	R2	296	50	6	78	23	11	14	0	0	0
358	T5	72	R3	267	59	5	77	18	8	7	0	0	0
359	T4	72	R4	325	59	6	22	14	13	12	0	0	0
360	T3	72	R5	295	54	8	21	14	12	10	0	0	0
361	T5	73	R1	247	52	8	114	22	9	17	0	0	0
362	T3	73	R2	300	57	6	23	13	12	12	0	1	0
363	T1	73	R3	264	56	8	108	23	7	16	0	0	0
364	T4	73	R4	267	56	7	93	21	13	13	0	0	0
365	T2	73	R5	309	59	7	86	23	6	16	0	1	0
366	T1	74	R1	312	48	5	72	21	13	13	0	0	0
367	T5	74	R2	320	63	6	25	15	13	15	0	0	0
368	T4	74	R3	317	49	5	62	22	13	12	0	0	0
369	T2	74	R4	307	50	5	76	22	10	13	0	0	0
370	T3	74	R5	275	56	7	112	23	10	16	0	0	0
371	T1	75	R1	306	56	5	22	14	14	11	0	0	0
372	T2	75	R2	295	65	8	127	22	6	19	0	0	0
373	T3	75	R3	275	56	9	140	22	10	22	0	0	0
374	T5	75	R4	267	61	7	123	22	10	19	0	0	0
375	T4	75	R5	320	59	7	24	15	13	12	0	0	0
376	T2	76	R1	280	50	7	23	15	12	14	0	0	0
377	T1	76	R2	260	55	6	22	13	11	12	0	0	0
378	T5	76	R3	290	64	6	22	13	13	14	0	0	0
379	T4	76	R4	322	53	7	89	21	12	12	0	0	0
380	T3	76	R5	x	x	x	x	x	x	x	x	x	x
381	T5	77	R1	251	54	7	91	22	11	13	0	0	0
382	T4	77	R2	250	62	7	88	20	10	12	0	0	0
383	T3	77	R3	x	x	x	x	x	x	x	x	x	x
384	T1	77	R4	280	53	7	88	21	11	15	0	0	0
385	T2	77	R5	303	58	7	90	22	10	11	0	0	0
386	T1	78	R1	280	54	4	22	12	11	11	0	0	0
387	T5	78	R2	305	54	5	72	22	14	11	0	0	0
388	T3	78	R3	305	60	4	21	14	11	14	0	0	0
389	T2	78	R4	327	50	6	82	23	13	15	0	0	0
390	T4	78	R5	295	56	7	23	13	10	10	0	0	0
391	T5	79	R1	250	49	7	30	25	13	11	0	0	0
392	T2	79	R2	310	46	6	86	22	11	18	0	0	0
393	T4	79	R3	305	48	6	84	21	7	15	0	0	0
394	T3	79	R4	x	x	x	x	x	x	x	x	x	x
395	T1	79	R5	290	64	6	22	13	13	14	0	0	0
396	T4	80	R1	305	54	6	77	22	12	14	0	0	0
397	T1	80	R2	300	57	6	23	13	7	12	0	0	0
398	T3	80	R3	310	61	7	22	15	9	13	0	1	0
399	T5	80	R4	305	59	6	23	16	14	13	0	0	0
400	T2	80	R5	307	55	7	93	22	7	12	0	0	0

Infected plants are highlighted in yellow.

Dead plants are highlighted in red.